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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 6, 2004, 09:59:31 ; Search time 21 Seconds
(without alignments)
2614.872 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	438.5	14.1	1524	2	T30337	polyprotein - Afri
2	437.5	14.1	343	1	A57014	prostasin (EC 3.4.
3	384.5	12.4	1004	2	T30338	oviductin (EC 3.4.
4	370.5	11.9	790	1	PLPG	plasmin (EC 3.4.21
5	369.5	11.9	812	1	PLMS	plasmin (EC 3.4.21
6	368.5	11.9	855	2	JC7731	membrane-bound arg
7	359.5	11.6	810	1	PLHU	plasmin (EC 3.4.21
8	359	11.6	810	2	I46260	plasmin (EC 3.4.21
9	356.5	11.5	812	1	PLBO	plasmin (EC 3.4.21
10	355.5	11.4	455	2	A61545	plasmin (EC 3.4.21
11	353	11.4	417	1	S00845	hepsin (EC 3.4.21.
12	351.5	11.3	810	2	B30848	plasmin (EC 3.4.21
13	342	11.0	4548	1	S00657	apoprotein(a) (EC
14	339	10.9	1420	2	A32869	apolipoprotein(a)
15	338	10.9	460	2	B61545	plasmin (EC 3.4.21
16	337.5	10.9	638	1	KQHUP	plasma kallikrein
17	336	10.8	270	2	S56160	mast cell tryptase
18	335	10.8	275	2	A32410	tryptase (EC 3.4.2
19	333	10.7	276	2	A38654	mast cell proteina
20	330.5	10.6	273	2	A47246	tryptase (EC 3.4.2
21	330	10.6	271	2	A25528	pancreatic elastas
22	329	10.6	275	2	A35863	tryptase (EC 3.4.2
23	329	10.6	275	2	B35863	tryptase (EC 3.4.2
24	328.5	10.6	274	2	JC4171	tryptase (EC 3.4.2
25	328	10.6	275	2	C35863	tryptase (EC 3.4.2
26	327.5	10.5	366	2	JE0105	testicular serine
27	326.5	10.5	625	1	KFHU1	coagulation factor
28	326.5	10.5	638	1	KQMSPL	plasma kallikrein
29	325.5	10.5	263	1	KYRTB	chymotrypsin (EC 3
30	325.5	10.5	638	1	KQRTPL	plasma kallikrein
31	325	10.5	416	1	S33777	hepsin (EC 3.4.21.
32	322.5	10.4	421	1	S11674	acrosin (EC 3.4.21
33	322	10.4	269	2	B26823	pancreatic elastas
34	322	10.4	269	2	A26823	pancreatic elastas
35	320.5	10.3	431	2	S47538	acrosin (EC 3.4.21
36	320	10.3	269	2	C26823	pancreatic elastas
37	320	10.3	271	1	ELRT2	pancreatic elastas
38	318.5	10.2	274	2	A45754	tryptase (EC 3.4.2
39	317.5	10.2	263	2	A21195	chymotrypsin (EC 3
40	317.5	10.2	761	2	JC5759	brain-specific ser
41	315.5	10.2	263	2	A31299	chymotrypsin (EC 3
42	315	10.1	1113	2	JE0315	low-density lipopr
43	313.5	10.1	245	1	KYBOA	chymotrypsin (EC 3
44	313	10.1	421	2	S29599	acrosin (EC 3.4.21
45	310.5	10.0	245	1	KYBOB	chymotrypsin (EC 3

ALIGNMENTS

RESULT 1
T30337
polyprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
C;Accession: T30337
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer
A;Reference number: Z20829
A;Accession: T30337
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1524 <YAN>
A;Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1
C;Superfamily: tryosin related polyprotein; trypsin homology

Query Match 14.1%; Score 438.5; DB 2; Length 1524;
Best Local Similarity 18.8%; Pred. No. 9.6e-23;
Matches 147; Conservative 97; Mismatches 211; Indels 327; Gaps 20;

```
Qy         59 GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE 118
              |:  |  ||  |::    ||| ||:|    |:|||||       :::  :|::|   ::
Db         61 GDAAVGGQPWTVSLKLNERHICGGSIVRKDMVVTAAHCVYPVTEIKVSHMTVIVGEYDQQ 120

Qy        119 GLSPGAEEVGVAALQ-LPRAYNHYSQGSDLALLQLAHP----TTHTPLCLPQPAHRFPFG 173
               :   : : |: ::  |       : | |:||: |:  |    :   |:||||   :   |
Db        121 VMDSQEQSIPVSHIEPHPNYRGDGNMGYDIALVFLSKPIIFGSQVQPICLPQVGEKIEAG 180

Qy        174 ASCWATGWD--QDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
                | ::||   ::  |   |: ::| ::   ||: :   :    | :     ||| |
Db        181 TLCVSSGWGRLEENGDLSPVLQEVKLPVVDNGTCHAVLEPIGHPVLDDT----MLCAGFP 236

Qy        232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSC----------AQEDAPVLLTN-- 278
              |    |||||||| :|    | |  || :|:  |           :|  :| : :
Db        237 EGGMDACQGDSGGPFVCRRRSGVWFLAGCVSWGLGCGRSWGAKQIIRSQSGSPAIFSRVS 296

Qy        279 ----------TAAHSS-------------------------WLQA---------- 288
                       |   ||                        |: |
Db        297 SVLDFLRPPKLTGGCSSKGRTITGKNGTVRYPLSGNYSINSVCRWMLAVQKAKTIEIRFL 356

Qy        289 ------------------------------------------------------- 288

Db        357 QLDIEDHATCTFDYLSFTVNEKMIRKVCGSTIPSPLIVRSNKVTVTFFSDGTFTGRGFEI 416

Qy        289 ----------------------------------RVQGAAFLAQSPET---------- 302
                                               |::  ::: ::||
Db        417 QFLAIPTKAASACGSAKILKKKGMIYSPNYPDPYPRLKTCSWIIEAPENHIVKLKFEDFN 476

Qy        303 ----------------------------------PEMSDEDSCV---------------- 312
                                               |  | |:: :
Db        477 VEYGHGCIYDAVEVYDGAEEKQLIARLCGYTLPLPISSPENTMLIRFKTDMENSYPGFKV 536
```

```
Qy        313 --------------------------------ACGSL---------RTAGPQAGAPSPWP 331
                                               ||          |  | :  :|: ||
Db        537 KFSFVPKEKQFSLPVDDTPTISMLHPRAIALDVCGMAPMTPKWWLPRIVGGEEASPNSWP 596

Qy        332 WEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLG--------TRPEEWGL 383
              |: ::       | ||::| : :|||||| |     |  |:|  |        :  :   :
Db        597 WQVQIFFLRTFHCEGAIISPQWILTAAHC-IRAAEPSYWTVIAGDHNRMLNESTEQIRNI 655

Qy        384 KQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE----RGW--VL 437
              | : :|  |        |:||| | :|: |   :||:||| |:  |           ||
Db        656 KTIRIHDNYNSETYDNDIALLYLEEPLDLNDFVRPVCLPEPEEVLTPASVCVVTGWGNTA 715

Qy        438 GRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAV--GEL------ 489
                :|  |:  ||                          |||  ::| ::   |||
Db        716 EDGQPALGLQQLQL----------------------PILDSIICNTSYYSGELTDHMLC 752

Qy        490 ---PS------CEGLSGAPLVHEVRGTWF-LAGLHSFGDACQGPARPAVFTALPAYEDWV 539
                 ||       |:| || ||| :     | : || |:|: |   ::| |:| :  :  |:
Db        753 AGFPSSKEKDACQGDSGGPLVCQNEKEQFSIYGLVSWGEGCGRVSKPGVYTKVRLFFTWI 812

Qy        540 SS 541
               :
Db        813 QN 814
```

RESULT 2
A57014
prostasin (EC 3.4.21.-) precursor - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C;Accession: A57014; A54866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of hum
A;Reference number: A57014; MUID:95286644; PMID:7768952
A;Accession: A57014
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-343 <RES>
A;Cross-references: GB:L41351; NID:g862304; PIDN:AAC41759.1; PID:g862305
A;Experimental source: prostate
A;Note: parts of this sequence were determined by protein sequencing
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification,
A;Reference number: A54866; MUID:94308140; PMID:8034638
A;Accession: A54866
A;Molecule type: protein
A;Residues: 45-64 <YUA>
C;Genetics:
A;Gene: GDB:PRSS8
A;Cross-references: GDB:676446; OMIM:600823
A;Map position: 16p11.2-16p11.2
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-44,45-343/Product: prostasin #status predicted <MAT>
F;33-44/Domain: prostasin light chain #status predicted <CHL>
F;45-343/Domain: prostasin heavy chain #status predicted <CHH>
F;45-281/Domain: trypsin homology <TRY>
F;323-341/Domain: transmembrane #status predicted <TMM1>
F;37-154,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F;85,134,238/Active site: His, Asp, Ser #status predicted
F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match   14.1%; Score 437.5; DB 1; Length 343;
  Best Local Similarity   35.3%; Pred. No. 2.1e-23;
  Matches 110; Conservative   48; Mismatches 109; Indels   45; Gaps   14;

```
Qy         51 PQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSV 110
              || :     : | |:|||| |:  :| |:| ||||:: |||:|||||       |  :: |
Db         41 PQARITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEV 98
```

```
Qy        111 VLGSLQREGLSPGAEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLC 162
              ||: | :  |   |:  |: |:  :|   ::  :||  |:|||||: | | :     |:|
Db         99 KLGAHQLDSYS---EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPIC 154

Qy        163 LPQPAHRFPFGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLS 218
              ||     || |  |  |||            |  |: | : |||| ||||:||   :
Db        155 LPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEP 214

Qy        219 NPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTN 278
              :  :  |:| |   | :  |||||||: |   :| |   ||:|:  :|   : | : |
Db        215 HFVQEDMVCAGYVEGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTL 273

Qy        279 TAAHSSWLQARV---QGAAFLAQSPETPEMSDEDSCVACGS------------LR----- 318
               ::::||:|::|   |        |:| | |  || : |||             ||
Db        274 ASSYASWIQSKVTELQPRVV----PQTQE-SQPDSNL-CGSHLAFSSAPAQGLLRPILFL 327

Qy        319 TAGPQAGAPSPW 330
              |   |  |||
Db        328 PLGLALGLLSPW 339
```

RESULT 3
T30338
oviductin (EC 3.4.21.-) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
C;Accession: T30338; A40242
R;Lindsay, L.L.; Wieduwilt, M.J.; Hedrick, J.L.
Biol. Reprod. 60, 989-995, 1999
A;Title: Oviductin, the Xenopus laevis oviductal protease that processes egg envelope gl
omposed of two protease and several CUB domains.
A;Reference number: Z20830; MUID:99184825; PMID:10084976
A;Accession: T30338
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1004 <LIN>
A;Cross-references: EMBL:U81291; NID:g1754713; PID:g1754714; PIDN:AAB53972.1
R;Hardy, D.M.; Hedrick, J.L.
Biochemistry 31, 4466-4472, 1992
A;Title: Oviductin. Purification and properties of the oviductal protease that processes
A;Reference number: A40242; MUID:92256375; PMID:1581303
A;Accession: A40242
A;Molecule type: protein
A;Residues: 46-73 <HAR>
C;Comment: This protease is found in oviductal secretory granules and is secreted to proc
C;Superfamily: oviductin; trypsin homology
C;Keywords: extracellular protein; hydrolase; serine proteinase

  Query Match   12.4%; Score 384.5; DB 2; Length 1004;
  Best Local Similarity   19.3%; Pred. No. 3.7e-19;
  Matches 155; Conservative   92; Mismatches 232; Indels 325; Gaps   25;

```
Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHC-FEKAAATELNSWSVVLGSLQREGLSP 122
              |: ||  |::| | | | |:||:   |||||||  ::     :    | :|    : |
Db         55 GQHPWTVSLKRNGKHFCGGTLVSHCHVLTAAHCLLDRNVKLYMR---VYIGEYD-QILKE 110

Qy        123 GAEEV--GVAALQLPRAYNHYSQGSDLALLQLAHPTTH----TPLCLPQPAHRFPFGASC 176
                |::   :   : |          |:|:| |    |       | ||| |   |  | |
Db        111 ETEQMFRVIEIFKHPNFNQSQPMNYDVAVLLLDGSVTFDENIQPACLPNPDDVFEPGDLC 170

Qy        177 WATGWDQDTSDA--PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGV 234
                 ||   | :   |  |: : | ::   :|  : : |    :|:     ::| |   |
Db        171 VTLGWGHLTENGILPVVLQEVYLPIVDLSSCLHVMSALKGTVVSS----YIVCAGFPEGG 226

Qy        235 QGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCA----------QEDAPVLLTNTAAH 282
              :  ||||||||:||    | ||  |: |:  |             :: :| : |:
Db        227 KDACQGDSGGPLLCQRRHGSWVLHGLTSWGMGCGRSWKNNVFLPHNRKGSPGIFTDIQKL 286

Qy        283 SSWLQARVQGAA---------------------------------------------- 294
               |: :::  |
Db        287 LGWVSSQLNTAVPNKNQESCSMQDGVLSGKSGELIFLKNPMSVTRTMSGAPGFSLSLKTC 346
```

```
Qy        295 --------------------FLA----------------------------------- 297
                              :||
Db        347 TSCLNFTHLDIESDFACNLDYLAIYTDSHRLIGKFCGDIPPRSLLISFSSIKLNFFSDFH 406

Qy        298 ------------------------------------QSPETPE----------------- 304
                                                 ||   ||
Db        407 ENRTGFVLYYSAVEPNTYPDSGCGSFAVLFEEGEIQSMNYPENYLSNSRCHWIIHGPSGS 466

Qy        305 ----------MSDEDSC-----------------VACG--------------------- 315
                       :   | |                  ||
Db        467 YIKLQFEDFALEPSDDCRSDYLAVYQDLAAEDKIETFCGFSLPAPVYSTTAVMHIKFSTD 526

Qy        316 -----------------SLRTAGPQAGAPS---------------------------- 328
                              ||     |   ||
Db        527 ERDNDKGFRATFTFVSPNSLVEDSRQGNMPSTNKKETTAQDSICGVSQVPPIFIYNSIAK 586

Qy        329 -------PWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLG----TR 377
                    |||   | : |:  | ||:::|  :|| | | : |:  : | |  |     |
Db        587 VEEAVPHSWPWHTSLQYAGEHVCDGAIIAENWILTTASCVLNRKFNDVWLVDPGIHDLLR 646

Qy        378 P--EEWGL-KQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE-- 432
              |   : || ||:| | :::     :|:||: | : :   : : |:|||      |
Db        647 PGHNQKGLVKQIIPHPSFSSQTNDFDIALVELDESLQFNSDIFPICLPGKTSELAPASLC 706

Qy        433 --RGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAA-PGGDGSPILPGMVCTSAVG-- 487
                || | | :     : ||   | :|   |||  :  |||    |   |:| : :|
Db        707 VVSGWSL-RGKEAEKSTKLQQREVPILTDDACSAHYIQNPGG----ITDRMLC-AGIGTG 760

Qy        488 -ELPSCEGLSGAPLV--HEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 544
               :  ||   ||:|||   | :| : : |: |:|  |:  ::| ::| :  : ||:  :
Db        761 QDNDSCSEQSGSPLVCLLEKKGIYTIFGIASWGVNCKENSKPGIYTKVSPFIDWIRQI-- 818

Qy        545 QVYFAEEPEPEAEPGSCLANISQP 568
                       :: |   :|:  |
Db        819 ----------MSDTGQIHSNLGDP 832
```

RESULT 4
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
R;Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A;Reference number: S03733
A;Accession: S03733
A;Molecule type: protein
A;Residues: 1-560 <SCH>
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03737
A;Molecule type: protein
A;Residues: 1-57 <BRU>
R;Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A;Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A;Reference number: A25834; MUID:85203907; PMID:3846533
A;Accession: A25834
A;Molecule type: protein
A;Residues: 450-790 <MAR>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F;1-790/Product: plasminogen #status predicted <PRO>
F;1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F;1-77/Domain: activation peptide #status predicted <APT>
F;78-560/Product: plasmin chain A #status predicted <ACH>
F;84-162/Domain: kringle homology <KR1>
F;166-243/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status experimental <MIN>
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status experimental <BCH>
F;561-783/Domain: trypsin homology <TRY>
F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305-
bonds: #status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted

  Query Match   11.9%; Score 370.5; DB 1; Length 790;
  Best Local Similarity 32.3%; Pred. No. 2.7e-18;
  Matches   90; Conservative   49; Mismatches 101; Indels   39; Gaps   12;

```
Qy         23 LYDFCIV--CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR- 73
              |:|:| |  |:|:           ||      ||:  :  |:  |   ::|  |||| |:|
Db        531 LFDYCDVPQCVTS----------SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY 580

Qy         74 RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
              |   | | |:|::  ||||| || ||:::   :|: |:||: :   |  | :|: |: |
Db        581 RYRGHFCGGTLISPEWVLTAKHCLEKSSSP--SSYKVILGAHEEYHLGEGVQEIDVSKL- 637

Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-A 188
                 :   |: :|:|||:|: |   |    | ||| | :       :|: |||| :
Db        638 ----FKEPSE-ADIALLKLSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYG 692

Qy        189 PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC 248
               | |:  || :|    ||         :|     |  || |   |    ||||||||::|
Db        693 AGLLKEARLPVIENKVCN------RYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVC 746

Qy        249 LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
               | | : :| |: |:   ||  : | :   :   :|::
Db        747 FEKDKYILQ-GVTSWGLGCALPNKPGVYVRVSRFVTWIE 784
```

RESULT 5
PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of th
A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514
A;Molecule type: mRNA
A;Residues: 1-812 <DEG>
A;Cross-references: GB:J04766; NID:g200402; PIDN:AAA50168.1; PID:g200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LI2>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin
mediately after dissociation from the clot. In the presence of the inhibitor, the activat
e inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. Tog
eful in treating solid tumors.
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va

```
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-812/Product: plasminogen #status predicted <PRO>
F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiostatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <MAT>
F;97-581/Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

  Query Match             11.9%;  Score 369.5;  DB 1;  Length 812;
  Best Local Similarity   32.7%;  Pred. No. 3.3e-18;
  Matches   93;  Conservative   45;  Mismatches  107;  Indels   39;  Gaps   11;

Qy          23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRRQ  75
               |||:| : :   |       |  :  :|| : |:  |  |       |  |||| |:| :
Db         551 LYDYCDIPLCASA--------SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR  602

Qy          76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ  133
                 | | |  |:|:|  |||||||| ||::  |   : |:||: :        :|: || |
Db         603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI  660

Qy         134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD  187
               |           |:|||:|: | | |    | ||| | :       |: |||   | |
Db         661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG  714

Qy         188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL  247
               | | |:  :| :|    || :       :|:|  :   || |   |    ||||||||::
Db         715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV  767

Qy         248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ  291
               | | | : :| |: |:   ||: : | :    :    |::  ::
Db         768 CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR  810


RESULT 6
JC7731
membrane-bound arginine-specific serine proteinase precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 03-Feb-2003
C;Accession: JC7731; JC7775
R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda,
J. Biochem. 130, 425-430, 2001
A;Title: Characterization of a membrane-bound arginine-specific serine protease from rat
A;Reference number: JC7731; MUID:21421307; PMID:11530019
A;Accession: JC7731
A;Molecule type: mRNA
A;Residues: 1-855 <KIS>
A;Cross-references: DDBJ:AB049189
A;Experimental source: strain Male, 7-week-old
R;Satomi, S.; Yamasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001
A;Title: A role for membrane-type serine protease (MT-SP1) in intestinal epithelial turn
A;Reference number: JC7775; PMID:11573963
A;Contents: Small intestine
A;Accession: JC7775
A;Molecule type: mRNA
A;Residues: 1-855 <SAT>
A;Cross-references: DDBJ:AB037898
C;Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease.
 of specific proteins or peptides on the brushborder membranes. It also participates in t
lial migration and/or cell loss.
C;Genetics:
A;Gene: mt-sp1
A;Map position: basolateral cell surface
C;Superfamily: membrane-bound arginine-specific serine proteinase
C;Keywords: protein digestion

  Query Match             11.9%;  Score 368.5;  DB 2;  Length 855;
  Best Local Similarity   32.2%;  Pred. No. 4.1e-18;
  Matches   82;  Conservative   43;  Mismatches  107;  Indels   23;  Gaps    7;

Qy          44 SFRKVQEPQGKAKRHGNTVPGEWPWQASVRRQG-AHICSGSLVADTWVLTAAHCFEKAAA 102
               || |   | :     |   |||||| |:   |  |:|  ||::  |:::||||:
Db         608 SFTK----QARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDETI 663

Qy         103 ---TELNSWSVVLGSL-QREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTH 158
                  ::   |:  || | | :  : | :|  :  :    ::| ::   |:|||:|  |  :
Db         664 FKYSDHTMWTAFLGLLDQSKRSASGVQEHKLKRIITHPSFNDFTFDYDIALLELEKPAEY 723

Qy         159 T----PLCLPQPAHRFPFGASCWATGWDQDTSDAPGT--LRNLRLRLISRPTCNCIYNQL 212
               :    |:|||   | || | : | |||         |   |:   :|:|:: ||
Db         724 STVVRPICLPDNTHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTC------- 776

Qy         213 HQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDA 272
               :  |     | |:| |   |    ||||||||:  :| ||   |||::|:   ||| :
Db         777 -EELLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEKDGRIFQAGVVSWGEGCAQRNK 835

Qy         273 PVLLTNTAAHSSWLQ 287
               | : |       |::
Db         836 PGVYTRIPEVRDWIK 850


RESULT 7
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiostatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A04
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibri
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <PET>
A;Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; PID:g387026
A;Experimental source: leukocyte; lung fibroblast
R;Malgaretti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Ta
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in liv
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
A;Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human pla
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
```

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:g190112; PIDN:AAA60124.1; PID:g387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:g190110; PIDN:AAA60123.1; PID:g190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
R;Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R;Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
A;Molecule type: protein
A;Residues: 581-810 <WI1>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla

A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
A;Molecule type: protein
A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <WI2>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
A;Molecule type: protein
A;Residues: 483-507,'E',509-604 <WI3>
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A;Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A;Reference number: A92125; MUID:73149248; PMID:4694729
A;Contents: annotation; active site
R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A;Reference number: A92048; MUID:69234739; PMID:4240117
A;Contents: annotation; active site
R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A;Reference number: A92382; MUID:82213905; PMID:6919539
A;Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A;Reference number: A92458; MUID:85054794; PMID:6094526
A;Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A;Title: Kringle domains of human angiostatin. Characterization of the anti-proliferativ
A;Reference number: A58811; MUID:97067211; PMID:8910613
A;Contents: annotation
R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (MM
A;Reference number: A58812; MUID:9548733; PMID:9548733
A;Contents: annotation
R;Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51488; PDB:2PK4
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A;Reference number: A51911; PDB:1PKR
A;Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R;Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A;Reference number: A52408; PDB:1PMK
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65244; PDB:1CEA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65245; PDB:1CEB
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Ar
A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmino
A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.I
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4
A;Reference number: A39483; MUID:92118803; PMID:1310033
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65803; PDB:1HPJ
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A65804; PDB:1HPK
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:94237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminoge
A;Reference number: A58817; MUID:94237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many oth
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU ar
d PIR:FGHUGB).
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately aft
rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor,
C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial condi
C;Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Tog
ting solid tumors.

```
C;Genetics:
A;Gene: GDB:PLG
A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q26-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-810/Product: plasminogen #status experimental <PRO>
F;20-96/Domain: activation peptide #status experimental <APT>
F;79-466/Product: angiostatin #status experimental <AST>
F;97-580,581-810/Product: plasmin #status experimental <MAT>
F;97-580/Domain: plasmin chain A #status experimental <CHA>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;550-580,581-810/Product: microplasmin #status experimental <MMT>

  Query Match             11.6%;  Score 359.5;  DB 1;  Length 810;
  Best Local Similarity   33.8%;  Pred. No. 1.6e-17;
  Matches   95;  Conservative   39;  Mismatches  104;  Indels   43;  Gaps   13;

Qy          23 LYDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVR 73
               |||:| |  |              ||    :|| : |:  |  |       |  |||| |:|
Db         551 LYDYCDVPQCAAP----------SF-DCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLR 599

Qy          74 -RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAAL 132
                | | | |:|:: ||||||||  ||:     :|: |:||: |   | |  :|: |: |
Db         600 TRFGMHFCGGTLISPEWVLTAAHCLEKSPRP--SSYKVILGAHQEVNLEPHVQEIEVSRL 657

Qy         133 QLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTS 186
               |          |:|||:|: |   |    | ||| | :        |: |||   | |
Db         658 FLE------PTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTF 711

Qy         187 DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPV 246
               | | |:  :| :|    ||           |:  :   || |   |    ||||||||:
Db         712 GA-GLLKEAQLPVIENKVCN------RYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPL 764

Qy         247 LCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
               :| | | : :| |: |:   ||: : | :    :   :|::
Db         765 VCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVTWIE 804


RESULT 8
I46260
plasmin (EC 3.4.21.7) precursor - western European hedgehog
C;Species: Erinaceus europaeus (western European hedgehog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C;Accession: I46260
R;Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprot
A;Reference number: I46259; MUID:96025778; PMID:7592597
A;Accession: I46260
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-810 <LAW>
A;Cross-references: EMBL:U33171; NID:g1046360; PID:g1046361
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;379-456/Domain: kringle homology <KR4>
F;482-561/Domain: kringle homology <KR5>
F;582-803/Domain: trypsin homology <TRY>

  Query Match             11.6%;  Score 359;  DB 2;  Length 810;
  Best Local Similarity   32.8%;  Pred. No. 1.8e-17;
  Matches   90;  Conservative   42;  Mismatches  112;  Indels   30;  Gaps   10;

Qy          23 LYDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV--PGEWPWQASVRRQGAH 78
               |:|:| :  |::  : :         :   ||:    | |  |  |  |||| |:|| | |
Db         552 LFDYCDIPHCVSPSSADCG------KPKVEPKKCPGRVGGCVAHPHSWPWQVSLRRFGQH 605

Qy          79 ICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRAY 138
               | |:|::  ||:|||||  || :   :  : ||||: |   |    :  ||  : |   |
Db         606 FCGGTLISPEWVVTAAHCLEKFSNPAI--YKVVLGAHQETRLERDVQIKGVTKMFL-EPY 662

Qy         139 NHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-APGTLR 193
                  :|:|||:|: |   |    | |||   :     : |: |||  :       | |:
Db         663 R-----ADIALLKLSSPAIITDKDHPACLPNSNYMVADRSLCYITGWGETKGTYGAGLLK 717

Qy         194 NLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDG 253
               :| :|    ||        |  |:   |   || |   |    ||||||||::| | |
Db         718 EAQLPVIENKVCN------RQSFLNGRVRSTELCAGHLAGGVDSCQGDSGGPLVCFEKDR 771

Qy         254 HWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
               : :| |: |:   ||:   | :    : : ||||
Db         772 YILQ-GVTSWGLGCARLTRPGVYVRVSRYVSWLQ 804


RESULT 9
PLBO
plasmin (EC 3.4.21.7) precursor - bovine
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
C;Accession: S45046; A25835; I45961; S03736
R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A;Description: Cloning and characterizatin of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BER>
A;Cross-references: EMBL:X79402; NID:g494962; PIDN:CAA55939.1; PID:g494963
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Dannegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rickl
Eur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasmi
A;Reference number: A25835; MUID:85203906; PMID:3846532
A;Accession: A25835
A;Molecule type: protein
A;Residues: 27-334,'D',336-515,'H',517-554,'L',556-812 <SCH>
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and b
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 706-743,'R',745-812 <MAL>
A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1; PID:g163552
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, b
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen acti
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
```

```
F;1-26/Domain: signal sequence #status predicted <SIG>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;27-812/Product: plasminogen #status experimental <PRO>
F;27-103/Domain: activation peptide #status experimental <APT>
F;104-583,584-812/Product: plasmin #status experimental <MAT>
F;104-583/Domain: plasmin chain A #status experimental <ACH>
F;110-188/Domain: kringle homology <KR1>
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
F;384-461/Domain: kringle homology <KR4>
F;485-564/Domain: kringle homology <KR5>
F;584-812/Domain: plasmin chain B #status experimental <BCH>
F;584-805/Domain: trypsin homology <TRY>
F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,33
 bonds: #status predicted
F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted

  Query Match             11.5%;  Score 356.5;  DB 1;  Length 812;
  Best Local Similarity   30.8%;  Pred. No. 2.7e-17;
  Matches   84;  Conservative   46;  Mismatches  112;  Indels   31;  Gaps   10;

Qy          24 YDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV--PGEWPWQASVRRQGAHI  79
               :|:| |  | :::            ||:  :   :  |  |  |  |||| |:||   |
Db         556 FDYCDVPQCESSFDCGKP-------KVEPKKCSGRIVGGCVSKPHSWPWQVSLRRSSRHF 608

Qy          80 CSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRAYN 139
               | |:|::  |||||||| :   |  |: : |:||:   :      :|: |:     | :
Db         609 CGGTLISPKWVLTAAHCLDNILA--LSFYKVILGAHNEKVREQSVQEIPVS-----RLFR 661

Qy         140 HYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-APGTLRN 194
                 || :|:|||:|: |   |     | ||| | :       |: |||  :       | |:
Db         662 EPSQ-ADIALLKLSRPAIITKEVIPACLPPPNYMVAARTECYITGWGETQGTFGEGLLKE 720

Qy         195 LRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGH 254
               | :|    ||         :|    :|  || |   |    ||||||||::| | | :
Db         721 AHLPVIENKVCN------RNEYLDGRVKPTELCAGHLIGGTDSCQGDSGGPLVCFEKDKY 774

Qy         255 WVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
               :| |: |:   ||: : | :    : :  |::
Db         775 ILQ-GVTSWGLGCARPNKPGVYVRVSPYVPWIE 806


RESULT 10
A61545
plasmin (EC 3.4.21.7) precursor - horse (fragments)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: A61545; S17527
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: A61545
A;Molecule type: protein
A;Residues: 1-33;34-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A;Title: Complete amino acid sequence of equine miniplasminogen.
A;Reference number: S17527; MUID:92052077; PMID:1946332
A;Accession: S17527
A;Molecule type: protein
A;Residues: 118-455 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
F;1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F;1-33/Domain: activation peptide (fragment) #status experimental <APT>
F;34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F;37-114/Domain: kringle homology <KR4>
F;118-455/Product: miniplasminogen #status experimental <MIN>
F;126-205/Domain: kringle homology <KR5>
F;226-455/Domain: plasmin chain B #status experimental <BCH>
F;226-448/Domain: trypsin homology <TRY>
F;267,310,405/Active site: His, Asp, Ser #status predicted

  Query Match             11.4%;  Score 355.5;  DB 2;  Length 455;
  Best Local Similarity   31.5%;  Pred. No. 1.6e-17;
  Matches   93;  Conservative   47;  Mismatches   92;  Indels   63;  Gaps   12;

Qy          23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQ--------GKAKRH-----GNTVPG----- 64
               |:|:| |                        ||        || |       |  | |
Db         196 LFDYCDV---------------------PQCESSPFDCGKPKVEPKKCSGRIVGGCVAIA 234

Qy          65 -EWPWQASVR-RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSP 122
                |||| |:| | | | | |:|::  |||||||| |:::    ::: ||||:     |:
Db         235 HSWPWQISLRTRFGRHFCGGTLISPEWVLTAAHCLERSSRP--STYKVVLGTHHELRLAA 292

Qy         123 GAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWA 178
               ||::: |: | |           :|:|||:|: |   |     | |||   :     | |:
Db         293 GAQQIDVSKLFLE------PSRADIALLKLSSPAIITQNVIPACLPPADYVVANWAECFV 346

Qy         179 TGW--DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQG 236
               |||   ||:|:| | |:  :| :|    ||          :|:   :   || |   |
Db         347 TGWGETQDSSNA-GVLKEAQLPVIENKVCN------RYEYLNGRVKSTELCAGHLVGGVD 399

Qy         237 PCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
               ||||||||::| | | : :| |: |:   ||: : | :    ::  :|::  :|
Db         400 SCQGDSGGPLVCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSSFINWIERIMQ 453


RESULT 11
S00845
hepsin (EC 3.4.21.-) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: S00845
R;Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane doma
A;Reference number: S00845; MUID:88209431; PMID:2835076
A;Accession: S00845
A;Molecule type: mRNA
A;Residues: 1-417 <LEY>
A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
C;Genetics:
A;Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted

  Query Match             11.4%;  Score 353;  DB 1;  Length 417;
  Best Local Similarity   35.0%;  Pred. No. 2.2e-17;
  Matches   85;  Conservative   32;  Mismatches  100;  Indels   26;  Gaps   10;

Qy          60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
               :|  | |||| |:|  |||:| |||::  ||||||||| :     |: | |  |:: :
Db         168 DTSLGRWPWQVSLRYDGAHLCGGSLLSGDWVLTAAHCFPERNRV-LSRWRVFAGAVAQ-- 224

Qy         120 LSPGAEEVGVAAL-----QLP-RAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHR 169
                ||    ::|| |:       || |  |      :|:||: |: |    |    |:|||
Db         225 ASPHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPAAGQA 284

Qy         170 FPFGASCWATGW--DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
                 |  |  |||   |       | |:  |: :||   ||          |  :| | |
Db         285 LVDGKICTVTGWGNTQYYGQQAGVLQEARVPIISNDVCN------GADFYGNQIKPKMFC 338

Qy         228 GG-PQPGVQGPCQGDSGGPVLC---LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHS 283
                | |: |:   |||||||| :|   :     |  ||:|: : ||    | : |  :
```

```
Db        339 AGYPEGGIDA-CQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQKPGVYTKVSDFR 397

Qy        284 SWL 286
              |:
Db        398 EWI 400
```

RESULT 12
B30848
plasmin (EC 3.4.21.7) precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: B32869; B30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: B32869
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-810 <TOM>
A;Cross-references: GB:J04697; NID:g342272; PIDN:AAA36901.1; PID:g342273
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-9/Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted

  Query Match 11.3%; Score 351.5; DB 2; Length 810;
  Best Local Similarity 32.5%; Pred. No. 5.9e-17;
  Matches 92; Conservative 45; Mismatches 99; Indels 47; Gaps 14;

```
Qy         23 LYDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVR 73
              |:|:| |  |  :          ||    :|| : |:  |  |       |  |||| |:|
Db        551 LFDYCDVPQCAAS----------SF-DCGKPQVEPKKCPGRVVGGCVAYPHSWPWQISLR 599

Qy         74 -RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAAL 132
               | | | | |:|:: |||||||| ||::      : |:||: :   | |  :|: |: :
Db        600 TRLGMHFCGGTLISPEWVLTAAHCLEKSSRPSF--YKVILGAHREVHLEPHVQEIEVSKM 657

Qy        133 QLPRAYNHYSQ--GSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQD 184
                     :|:   :|:|||:|: |   |    | ||| | :       |: |||   |
Db        658 --------FSEPARADIALLKLSSPAIITDKVIPACLPSPNYVVADRTECFITGWGETQG 709

Qy        185 TSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGG 244
              |  | | |:  || :|    ||          |:   :   || |   |    |||||||
Db        710 TYGA-GLLKEARLPVIENKVCN------RYEFLNGTVKTTELCAGHLAGGTDSCQGDSGG 762

Qy        245 PVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              |::| | | : :| |: |:   ||: : | :    :   :|::
Db        763 PLVCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVTWIE 804
```

RESULT 13
S00657
apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N;Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C;Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scan
Nature 330, 132-137, 1987
A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A;Reference number: S00657; MUID:88039109; PMID:3670400
A;Accession: S00657
A;Molecule type: mRNA
A;Residues: 1-4548 <MCL>
A;Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620
R;Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.;
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A;Reference number: A28017; MUID:87204109; PMID:3472206
A;Accession: A28017
A;Molecule type: protein
A;Residues: 20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-318
X',4396-4401 <EAT>
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A;Title: 5' control regions of the apolipoprotein(a) gene and members of the related plas
A;Reference number: A47277; MUID:93165698; PMID:7679504
A;Accession: A47277
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: GB:L07899; NID:g967973; PID:g967974
R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Saccor
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipopro
A;Reference number: A47233; MUID:93087573; PMID:1454851
A;Accession: I60906
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RE2>
A;Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; PID:g553188
A;Note: apo(a) gene 1 (nomenclature of reference I52415)
A;Accession: A47233
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RE5>
A;Cross-references: GB:M90079; NID:g178784; PIDN:AAA35546.1; PID:g553187
R;Ichinose, A.
Biochemistry 31, 3113-3118, 1992
A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated wit
A;Reference number: I52415; MUID:92207924; PMID:1554698
A;Accession: I52415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RE3>
A;Cross-references: GB:M86877; NID:g178780; PIDN:AAB49909.1; PID:g553185
A;Note: apo(a) gene 1 (nomenclature of reference I52415)
A;Accession: I65286
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RE4>
A;Cross-references: GB:M86878; NID:g178782; PIDN:AAA51749.1; PID:g553186
C;Genetics:
A;Gene: GDB:LPA
A;Cross-references: GDB:120699; OMIM:152200
A;Map position: 6q26-6q27
A;Note: several genes closely linked on chromosome 6 are identical in the first coding ex
rs of kringle repeats
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-4548/Product: apolipoprotein(a) #status experimental <MAT>
F;28-105/Domain: kringle homology <KR1>
F;142-219/Domain: kringle homology <KR2>
F;256-333/Domain: kringle homology <KR3>
F;370-447/Domain: kringle homology <KR4>
F;484-561/Domain: kringle homology <KR5>
F;598-675/Domain: kringle homology <KR6>
F;712-789/Domain: kringle homology <KR7>
F;826-903/Domain: kringle homology <KR8>
F;940-1017/Domain: kringle homology <KR9>
F;1054-1131/Domain: kringle homology <KR10>
F;1168-1245/Domain: kringle homology <KR11>
F;1282-1359/Domain: kringle homology <KR12>
F;1396-1473/Domain: kringle homology <KR13>

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F;1510-1587/Domain: kringle homology <KR14>
F;1624-1701/Domain: kringle homology <KR15>
F;1738-1815/Domain: kringle homology <KR16>
F;1852-1929/Domain: kringle homology <KR17>
F;1966-2043/Domain: kringle homology <KR18>
F;2080-2157/Domain: kringle homology <KR19>
F;2194-2271/Domain: kringle homology <KR20>
F;2308-2385/Domain: kringle homology <KR21>
F;2422-2499/Domain: kringle homology <KR22>
F;2536-2613/Domain: kringle homology <KR23>
F;2650-2727/Domain: kringle homology <KR24>
F;2764-2841/Domain: kringle homology <KR25>
F;2878-2955/Domain: kringle homology <KR26>
F;2992-3069/Domain: kringle homology <KR27>
F;3106-3183/Domain: kringle homology <KR28>
F;3220-3297/Domain: kringle homology <KR29>
F;3334-3411/Domain: kringle homology <KR30>
F;3448-3525/Domain: kringle homology <KR31>
F;3562-3639/Domain: kringle homology <KR32>
F;3676-3753/Domain: kringle homology <KR33>
F;3782-3859/Domain: kringle homology <KR34>
F;3896-3973/Domain: kringle homology <KR35>
F;4010-4087/Domain: kringle homology <KR36>
F;4124-4201/Domain: kringle homology <KR37>
F;4228-4307/Domain: kringle homology <KR38>
F;4328-4541/Domain: trypsin homology <TRY>

  Query Match             11.0%;  Score 342;  DB 1;  Length 4548;
  Best Local Similarity   29.4%;  Pred. No. 2e-15;
  Matches   83;  Conservative   50;  Mismatches  103;  Indels   46;  Gaps   10;

Qy         23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV-------PGEWPWQASVR-R 74
              |:|:|          :: |   |     :|| : |:   ::        |  ||||.|:| |
Db       4298 LFDYC---------DIPLCASSSFDCGKPQVEPKKCPGSIVGGCVAHPHSWPWQVSLRTR 4348

Qy         75 QGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQL 134
               | | | |:|::  |||||||| :|::    :|: |:||: |    |    :|: |: | |
Db       4349 FGKHFCGGTLISPEWVLTAAHCLKKSSRP--SSYKVILGAHQEVNLESHVQEIEVSRLFL 4406

Qy        135 PRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-AP 189
                        :|:|||:|: |    |     | ||| | :        |: ||| :
Db       4407 EPTQ------ADIALLKLSRPAVITDKVMPACLPSPDYMVTARTECYITGWGETQGTFGT 4460

Qy        190 GTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCL 249
              | |:  :| :|     ||   |  :   ||:                    |||||||::|
Db       4461 GLLKEAQLLVIENEVCN-HYKYICAEHLARGT--------------DSCQGDSGGPLVCF 4505

Qy        250 EPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
              | | : :| |: |:   ||: : | :    :   :|::  ::
Db       4506 EKDKYILQ-GVTSWGLGCARPNKPGVYARVSRFVTWIEGMMR 4546


RESULT 14
A32869
apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
C;Accession: A32869; A30848
R;Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A;Reference number: A32869; MUID:89174660; PMID:2925643
A;Accession: A32869
A;Molecule type: mRNA
A;Residues: 1-1420 <TOM>
A;Cross-references: GB:J04635; NID:g342072; PIDN:AAA36833.1; PID:g342073
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F;50-127/Domain: kringle homology <KR1>
F;164-241/Domain: kringle homology <KR2>
F;278-355/Domain: kringle homology <KR3>
F;392-469/Domain: kringle homology <KR4>
F;506-583/Domain: kringle homology <KR5>
F;620-697/Domain: kringle homology <KR6>
F;726-803/Domain: kringle homology <KR7>
F;840-917/Domain: kringle homology <KR8>
F;954-1031/Domain: kringle homology <KR9>
F;1068-1145/Domain: kringle homology <KR10>
F;1191-1413/Domain: trypsin homology <TRY>

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Qy         50 EPQGKAKRHGNTV-------PGEWPWQASVR-RQGAHICSGSLVADTWVLTAAHCFEKAA 101
              :|| : |:   ::        |  |||| |:| | | | | |:|::  ||||||  | |  :
Db       1179 KPQVEPKKCPGSIVGGCVAHPHSWPWQVSLRTRFGKHFCGGTLISPEWVLTAACCLETFS 1238

Qy        102 ATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT-- 159
                  : |:||: |    |     :|: |: | |          |:|:|||:|: |    |
Db       1239 RPSF--YKVILGAHQEVNLESHVQEIEVSRLFLEPI------GADIALLKLSRPAIITDK 1290

Qy        160 --PLCLPQPAHRFPFGASCWATGW--DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQR 215
                | ||| | :        |: |||   | |  | | |:  :| :|     ||       |
Db       1291 VIPACLPSPNYVITAWTECYITGWGETQGTFGA-GLLKEAQLHVIENTVCN------HYE 1343

Qy        216 HLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVL 275
              |:   :   || |    |    ||||:||||:| : |  ::  || |:   ||  : | :
Db       1344 FLNGRVKSTELCAGHLAGGTDRCQGDNGGPVVCFDKD-KYILRGITSWGPGCACPNKPGV 1402

Qy        276 LTNTAAHSSWLQ 287
                ::  :|::
Db       1403 YVRVSSFVTWIE 1414


RESULT 15
B61545
plasmin (EC 3.4.21.7) precursor - sheep (fragments)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
C;Accession: B61545; S28200
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: B61545
A;Molecule type: protein
A;Residues: 1-37;38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995; PMID:1492092
A;Accession: S28200
A;Molecule type: protein
A;Residues: 118-460 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology;
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z
F;1-37,38-117,118-460/Product: plasminogen (fragments) #status experimental <PRO>
F;1-37/Domain: activation peptide (fragment) #status experimental <APT>
F;38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
F;41-118/Domain: kringle homology <KR4>
F;118-460/Product: miniplasminogen #status experimental <MIN>
F;132-211/Domain: kringle homology <KR5>
F;226-460/Domain: plasmin chain B #status experimental <BCH>
F;231-453/Domain: trypsin homology <TRY>
F;272,315,410/Active site: His, Asp, Ser #status predicted

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Qy         23 LYDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV--PGEWPWQASVRRQG-A 77
              |:|:| :  | :::             ||:  :  |:  |  |  |  |||| |:||:
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Qy          78 HICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRA 137
               | | |:|::  |||||||| :          ::|:||:           :|: |: | |
Db         255 HFCGGTLISPEWVLTAAHCLDSILGPSF--YTVILGAHYEMAREASVQEIPVSRLFLE-- 310

Qy         138 YNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-APGTL 192
                     :|:|||:|: |   |    | ||| | :        |: ||| :        | |
Db         311 ----PSRADIALLKLSSPAVITDEVIPACLPSPNYVVADKTVCYITGWGETQGTFGVGRL 366

Qy         193 RNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPD 252
               :  || :|    ||          :|:   :   || |   |    ||||||||::| | |
Db         367 KEARLPVIENKVCN------RYEYLNGRVKSTELCAGDLAGGTDSCQGDSGGPLVCFEKD 420

Qy         253 GHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
                : :| |: |:   ||: : | :    : :  |::
Db         421 KYILQ-GVTSWGLGCARPNKPGVYVRVSTYVPWIE 454


Search completed: January  6, 2004, 10:03:10
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 6, 2004, 10:02:42 ; Search time 37 Seconds
(without alignments)
3096.382 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 733937 seqs, 200641211 residues

Total number of hits satisfying chosen parameters: 733937

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3108	100.0	571	10	US-09-978-295A-132	Sequence 132, App
2	3108	100.0	571	10	US-09-978-697-132	Sequence 132, App
3	3108	100.0	571	10	US-09-978-192A-132	Sequence 132, App
4	3108	100.0	571	10	US-09-999-832A-132	Sequence 132, App
5	3108	100.0	571	11	US-09-978-189-132	Sequence 132, App
6	3108	100.0	571	11	US-09-978-608A-132	Sequence 132, App
7	3108	100.0	571	11	US-09-978-585A-132	Sequence 132, App
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35	3108	100.0	571	12	US-10-164-728A-132	Sequence 132, App
36	3108	100.0	571	12	US-10-165-067A-132	Sequence 132, App
37	3108	100.0	571	12	US-10-145-124A-132	Sequence 132, App
38	3108	100.0	571	12	US-10-160-502A-132	Sequence 132, App
39	3108	100.0	571	12	US-10-165-247A-132	Sequence 132, App
40	3108	100.0	571	12	US-09-978-194A-132	Sequence 132, App
41	3108	100.0	571	12	US-09-978-681A-132	Sequence 132, App
42	3108	100.0	571	12	US-09-999-829A-132	Sequence 132, App
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ALIGNMENTS

RESULT 1
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; Sequence 132, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085697

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
US-09-978-697-132
; Sequence 132, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
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; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 10; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
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Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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RESULT 3
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; Sequence 132, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
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Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 4
US-09-999-832A-132
; Sequence 132, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 10; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
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Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
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Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

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Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 5
US-09-978-189-132
; Sequence 132, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
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Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 6
US-09-978-608A-132
; Sequence 132, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 132
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-132

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  Query Match            100.0%;  Score 3108;  DB 11;  Length 571;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-245;
  Matches  571;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              ||||||||||||||||||||||||||||||
Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 7
US-09-978-585A-132
; Sequence 132, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 132
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-132

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 8
US-09-978-191A-132
; Sequence 132, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
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; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR FILING DATE: 1998-04-22
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; PRIOR APPLICATION NUMBER: 60/082700
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

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RESULT 9
US-09-978-403A-132
; Sequence 132, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C17
;  CURRENT APPLICATION NUMBER: US/09/978,403A
;  CURRENT FILING DATE:  2002-03-19
;  PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
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Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
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Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 10
US-09-978-564A-132
; Sequence 132, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 3108; DB 11; Length 571;
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Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
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Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLC 420
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Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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RESULT 11
US-09-999-833A-132
; Sequence 132, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
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Qy          61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Db          61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy         121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
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Db         121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy         181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db         181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

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Qy         361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Db         361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy         421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db         421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

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RESULT 12
US-09-981-915A-132
; Sequence 132, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

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Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 13
US-09-978-824-132
; Sequence 132, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
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Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
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Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
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RESULT 14
US-09-918-585A-132
; Sequence 132, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
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Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
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Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
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Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
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Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLC 420
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Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
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Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
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RESULT 15
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; Sequence 132, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 3108; DB 11; Length 571;
Best Local Similarity 100.0%; Pred. No. 4.4e-245;
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GenCore version 5.1.6

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Title: US-09-978-194A-132
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Scoring table: BLOSUM62
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	447	14.4	284	4	US-09-387-375-7	Sequence 7, Appli
3	447	14.4	316	4	US-09-387-375-9	Sequence 9, Appli
4	446	14.4	315	4	US-09-386-653A-9	Sequence 9, Appli
5	429.5	13.8	299	3	US-08-944-483-66	Sequence 66, Appl
6	422	13.6	319	4	US-09-386-642-12	Sequence 12, Appl
7	422	13.6	328	4	US-09-386-642-11	Sequence 11, Appl
8	400	12.9	317	4	US-09-386-629-7	Sequence 7, Appli
9	388	12.5	327	4	US-09-386-629-8	Sequence 8, Appli
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11	370.5	11.9	790	4	US-08-991-761A-13	Sequence 13, Appl
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ALIGNMENTS

RESULT 1
US-09-386-653A-7
; Sequence 7, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-386-653A-7

Query Match 14.4%; Score 449; DB 4; Length 290;
Best Local Similarity 37.1%; Pred. No. 2.4e-31;
Matches 89; Conservative 44; Mismatches 87; Indels 20; Gaps 6;

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RESULT 2
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; Sequence 7, Application US/09387375
; Patent No. 6485957
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Qi, Jenson

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;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION: Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/09/387,375
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 284
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-387-375-7

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RESULT 3
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; Sequence 9, Application US/09387375
; Patent No. 6485957
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT: Qi, Jenson
;  TITLE OF INVENTION: DNA Encoding the Human Serine
;  TITLE OF INVENTION: Protease EOS
;  FILE REFERENCE: ORT-1031
;  CURRENT APPLICATION NUMBER: US/09/387,375
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of EOS zymogen fusion gene
US-09-387-375-9

  Query Match             14.4%;  Score 447;  DB 4;  Length 316;
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Qy        124 AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT 179
                | |  : ||  |:      |||||||  |   :    |:||| |  | | |  |  |
Db        119 TLSVPVRRVLLPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRVT 178

Qy        180 GWDQDTSDAPGT-------LRNLRLRLISRPTCNCIYN------QLHQRHLSNPARPGML 226
              ||    |  ||        |: :|: |:   ||: :|:      |  :  |     || |
Db        179 GWG---SLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERIVL-----PGSL 230

Qy        227 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
              | |   | :  |||||||: ||:  | ||  |::|:   ||  : | : |: | :| |:
Db        231 CAGYPQGHKDACQGDSGGPLTCLQ-SGSWVLVGVVSWGKGCALPNRPGVYTSVATYSPWI 289

Qy        287 QARVQGAA 294
                ||||   |
Db        290 QARVTSNA 297


RESULT 4
US-09-386-653A-9
; Sequence 9, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
;  APPLICANT: Andrade-Gordon, Patricia
;  APPLICANT:  Darrow, Andrew
;  APPLICANT:  Qi, Jian-shen
;  TITLE OF INVENTION: DNA encoding the novel human serine
;  TITLE OF INVENTION:  protease T
;  FILE REFERENCE: ORT-1032
;  CURRENT APPLICATION NUMBER: US/09/386,653A
;  CURRENT FILING DATE:  1999-08-31
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 315
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
;   OTHER INFORMATION: of Protease T in a zymogen activation construct
US-09-386-653A-9

  Query Match             14.4%;  Score 446;  DB 4;  Length 315;
  Best Local Similarity   37.3%;  Pred. No. 5e-31;
  Matches   88;  Conservative   43;  Mismatches   85;  Indels   20;  Gaps    6;

Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
              |||||| |::| |:| | |||:|: |||||||||   : | |  : |:|||: |     |
Db         61 GEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSL--YQVLLGARQLVQPGPH 118

Qy        124 AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT 179
                |  . |  ::    |   :  :|:||::|  |   |    |:||| |:  |  | :|| |
Db        119 AMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVT 178

Qy        180 GW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQ-----LHQRHLSNPARPGMLCGGP 230
              ||     ::|     |  |: | : :|  | || :|::         : :  |     ||| |
Db        179 GWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKN----DMLCAGF 234

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
              : | :  |:||||||::||     |:|||:||:   ||::: | :     || :|:
Db        235 EEGKKDACKGDSGGPLVCLVGQS-WLQAGVISWGEGCARQNRPGVYIRVTAHHNWI 289


RESULT 5
US-08-944-483-66
; Sequence 66, Application US/08944483
; Patent No. 6232456
;  GENERAL INFORMATION:
;    APPLICANT:  COHEN, MAURICE
;    APPLICANT:  COLPITTS, TRACEY L.
;    APPLICANT:  FRIEDMAN, PAULA N.
;    APPLICANT:  GRANADOS, EDWARD N.
;    APPLICANT:  KLASS, MICHAEL R.
;    APPLICANT:  RUSSELL, JOHN C.
;    APPLICANT:  STEWART, KENT D.
;    APPLICANT:  STROUPE, STEVEN D.
;    TITLE OF INVENTION:  NOVEL SERINE PROTEASE REAGENTS
```

```
;    TITLE OF INVENTION:  AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
;    TITLE OF INVENTION:  OF THE PROSTATE
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Abbott Laboratories
;      STREET:  100 Abbott Park Road
;      CITY:  Abbott Park
;      STATE:  IL
;      COUNTRY:  USA
;      ZIP:  60064-3500
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,483
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Becker, Cheryl L.
;      REGISTRATION NUMBER:  35,441
;      REFERENCE/DOCKET NUMBER:  6183.US.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  847/935-1729
;      TELEFAX:  847/938-2623
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  299 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6232456e
US-08-944-483-66

  Query Match             13.8%;  Score 429.5;  DB 3;  Length 299;
  Best Local Similarity   35.6%;  Pred. No. 1.3e-29;
  Matches  108;  Conservative   47;  Mismatches  103;  Indels   45;  Gaps   14;

Qy         60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
              : | |:|||| |:  :| |:| |||:: |||:|||||       |  :: | ||: | :
Db          6 SAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEVKLGAHQLDS 63

Qy        120 LSPGAEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLCLPQPAHRFP 171
              |   |:  |: |:  :|   ::  :||  |:|||||: | | :    |:|||     ||
Db         64 YS---EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFP 119

Qy        172 FGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
              | |  |||          |  |: | : |||| ||||:||   :    :  :|:|
Db        120 NGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVC 179

Qy        228 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              |   | :  ||||||||: |   :| |    ||:|:  :|   : | : |  ::::||:|
Db        180 AGYVEGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQ 238

Qy        288 ARV---QGAAFLAQSPETPEMSDEDSCVACGS------------LR-----TAGPQAGAP 327
              ::|   |          |:| | |  || : |||            ||        |  |
Db        239 SKVTELQPRVV----PQTQE-SQPDSNL-CGSHLAFSSAPAQGLLRPILFLPLGLALGLL 292

Qy        328 SPW 330
              |||
Db        293 SPW 295


RESULT 6
US-09-386-642-12
; Sequence 12, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Zymogen Activation System
;  FILE REFERENCE: ORT-1028
;  CURRENT APPLICATION NUMBER: US/09/386,642
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;   OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-12

  Query Match             13.6%;  Score 422;  DB 4;  Length 319;
  Best Local Similarity   37.3%;  Pred. No. 6.4e-29;
  Matches  100;  Conservative   46;  Mismatches   94;  Indels   28;  Gaps   12;

Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
              |:|||| |:  :| |:| ||||:: |||:|||||       |  :: | ||: | :  |
Db         52 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEVKLGAHQLDSYS-- 107

Qy        124 AEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
              |:  |: |:  :|   ::  :||  |:|||||: | | :    |:|||     || |
Db        108 -EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLH 165

Qy        176 CWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
              |  |||          |  |: | : |||| ||||:||   :    :  :|:| |
Db        166 CTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYV 225

Qy        232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARV- 290
              | :  ||||||||: |   :| |    ||:|:  :|   : | : |  ::::||:|::|
Db        226 EGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVT 284

Qy        291 --QGAAFLAQSPETPEMSDEDSCVACGS 316
                |         |:| | |  || : |||
Db        285 ELQPRVV----PQTQE-SQPDSNL-CGS 306


RESULT 7
US-09-386-642-11
; Sequence 11, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Zymogen Activation System
;  FILE REFERENCE: ORT-1028
;  CURRENT APPLICATION NUMBER: US/09/386,642
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
;   OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11

  Query Match             13.6%;  Score 422;  DB 4;  Length 328;
  Best Local Similarity   37.3%;  Pred. No. 6.6e-29;
  Matches  100;  Conservative   46;  Mismatches   94;  Indels   28;  Gaps   12;

Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
              |:|||| |:  :| |:| ||||:: |||:|||||       |  :: | ||: | :  |
Db         61 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEVKLGAHQLDSYS-- 116
```

```
Qy        124 AEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
Db        117 -EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLH 174

Qy        176 CWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
Db        175 CTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYV 234

Qy        232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARV- 290
Db        235 EGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASWIQSKVT 293

Qy        291 --QGAAFLAQSPETPEMSDEDSCVACGS 316
Db        294 ELQPRVV----PQTQE-SQPDSNL-CGS 315


RESULT 8
US-09-386-629-7
; Sequence 7, Application US/09386629
; Patent No. 6426199
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew L.
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Idenification and Characterization of the complementary
;  TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
;  FILE REFERENCE: ORT-1030
;  CURRENT APPLICATION NUMBER: US/09/386,629
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-386-629-7

  Query Match             12.9%;  Score 400;  DB 4;  Length 317;
  Best Local Similarity   30.8%;  Pred. No. 5.3e-27;
  Matches   99;  Conservative   57;  Mismatches  123;  Indels   42;  Gaps   11;

Qy         27 CIVCITTYAINVSLMWLSFRKVQEPQ--GKAKRHGNTVPG------EWPWQASVRRQGAH 78
Db         14 CLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTH 73

Qy         79 ICSGSLVADTWVLTAAHCFEKAAATELNS---WSVVLGSLQREGLSPGAEEVGVAALQLP 135
Db         74 HCAGSLLTSRWVITAAHCFK----DNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE-P 128

Qy        136 RAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW----DQDT 185
Db        129 HPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVP 188

Qy        186 SDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGP 245
Db        189 LPHPQTLQKLKVPIIDSEVCSHLY---WRGAGQGPITEDMLCAGYLEGERDACLGDSGGP 245

Qy        246 VLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEM 305
Db        246 LMC-QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQ----- 299

Qy        306 SDEDSCVACGSLRTAGPQAGA 326
Db        300 -------GGGALRAPSQGSGA 313


RESULT 9
US-09-386-629-8
; Sequence 8, Application US/09386629
; Patent No. 6426199
; GENERAL INFORMATION:
;  APPLICANT: Darrow, Andrew L.
;  APPLICANT: Qi, Jenson
;  APPLICANT: Andrade-Gordon, Patricia
;  TITLE OF INVENTION: Idenification and Characterization of the complementary
;  TITLE OF INVENTION: DNA encoding the novel human serine protease C-E
;  FILE REFERENCE: ORT-1030
;  CURRENT APPLICATION NUMBER: US/09/386,629
;  CURRENT FILING DATE: 1999-08-31
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 327
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: C-E catalytic
;   OTHER INFORMATION: domain fusion protien
US-09-386-629-8

  Query Match             12.5%;  Score 388;  DB 4;  Length 327;
  Best Local Similarity   32.7%;  Pred. No. 6.2e-26;
  Matches   90;  Conservative   49;  Mismatches  102;  Indels   34;  Gaps    9;

Qy         65 EWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS---WSVVLGSLQREGLS 121
Db         62 EWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFK----DNLNKPYLFSVLLGAWQLGNPG 117

Qy        122 PGAEEVGVAALQLPRAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
Db        118 SRSQKVGVAWVE-PHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTH 176

Qy        176 CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
Db        177 CWISGWGSIQDGVPLPHPQTLQKLKVPIIDSEVCSHLY---WRGAGQGPITEDMLCAGYL 233

Qy        232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
Db        234 EGERDACLGDSGGPLMC-QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQ 292

Qy        292 GAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGA 326
Db        293 GVQLRGRAQ-----------GGGALRAPSQGSGA 315


RESULT 10
US-09-644-600-10
; Sequence 10, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
;  APPLICANT: O'Brien, Timothy J.
;  APPLICANT:  Tanimoto, Hirotoshi
;  TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
;  TITLE OF INVENTION:  Overexpressed in Carcinomas
;  FILE REFERENCE: D6064CIP/D
;  CURRENT APPLICATION NUMBER: US/09/644,600
;  CURRENT FILING DATE:  2000-08-23
;  PRIOR APPLICATION NUMBER: 09/421,213
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: 09/027,337
;  PRIOR FILING DATE: 1998-02-20
;  NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
;   LENGTH: 902
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: Epithin
US-09-644-600-10

  Query Match             12.1%;  Score 375;  DB 4;  Length 902;
  Best Local Similarity   33.3%;  Pred. No. 3.4e-24;
  Matches   92;  Conservative   38;  Mismatches  114;  Indels   32;  Gaps    9;
```

```
Qy          44 SFRKVQEPQGKAKRHGNTVPGEWPWQASVRRQG-AHICSGSLVADTWVLTAAHCFE---K 99
Db         608 SFTK----QARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDDKN 663

Qy         100 AAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPR-----AYNHYSQGSDLALLQL-- 152
Db         664 FKYSDYTMWTAFLGLLDQSKRSAS----GVQELKLKRIITHPSFNDFTFDYDIALLELEK 719

Qy         153 --AHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSDAPGT--LRNLRLRLISRPTCNCI 208
Db         720 SVEYSTVVRPICLPDATHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEDL 779

Qy         209 YNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCA 268
Db         780 MPQ--------QITPRMMCVGFLSGGVDSCQGDSGGPLSSAEKDGRMFQAGVVSWGEGCA 831

Qy         269 QEDAPVLLTNTAAHSSWLQARVQG-AAFLAQSPETP 303
Db         832 QRNKPGVYTRLPCSSGLDQRAHWGIAAWTDSRPQTP 867
```

RESULT 11
US-08-991-761A-13
; Sequence 13, Application US/08991761A
; Patent No. 6576609
; GENERAL INFORMATION:
; APPLICANT: Soff, Gerald
; APPLICANT: Gately, Stephen
; APPLICANT: Twardowski, Przemyslaw
; TITLE OF INVENTION: "Methods and Compositions for Generating
; TITLE OF INVENTION: Angiostatin"
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln St., Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: USA
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,761A
; FILING DATE:
; CLASSIFICATION: 1642
; ATTORNEY/AGENT INFORMATION:
; NAME: Crook, Wannell M.
; REGISTRATION NUMBER: 31,071
; REFERENCE/DOCKET NUMBER: 3501-16-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 790 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-991-761A-13

Query Match 11.9%; Score 370.5; DB 4; Length 790;
Best Local Similarity 32.3%; Pred. No. 7.1e-24;
Matches 90; Conservative 49; Mismatches 101; Indels 39; Gaps 12;

```
Qy          23 LYDFCIV-CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR- 73
Db         531 LFDYCDVPQCVTS----------SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY 580

Qy          74 RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
Db         581 RYRGHFCGGTLISPEWVLTAKHCLEKSSSP--SSYKVILGAHEEYHLGEGVQEIDVSKL- 637

Qy         134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-A 188
Db         638 ----FKEPSE-ADIALLKLSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYG 692

Qy         189 PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC 248
Db         693 AGLLKEARLPVIENKVCN------RYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVC 746

Qy         249 LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
Db         747 FEKDKYILQ-GVTSWGLGCALPNKPGVYVRVSRFVTWIE 784
```

RESULT 12
US-08-248-629A-1
; Sequence 1, Application US/08248629A
; Patent No. 5639725
; GENERAL INFORMATION:
; APPLICANT: Folkman, Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50
; COMPUTER: MacIntosh
; OPERATING SYSTEM: 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,629A
; FILING DATE: 04/26/94
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larry W. Stults, Ph.D.
; REGISTRATION NUMBER: 34,025
; REFERENCE/DOCKET NUMBER: 05213-0120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-818-3700
; TELEFAX: 404-818-3799
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 812
; TYPE: amino acid
; TOPOLOGY: linear
US-08-248-629A-1

Query Match 11.9%; Score 369.5; DB 1; Length 812;
Best Local Similarity 32.7%; Pred. No. 9e-24;
Matches 93; Conservative 45; Mismatches 107; Indels 39; Gaps 11;

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Qy          23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRQ 75
Db         551 LYDYCDIPLCASA--------SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR 602

Qy          76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
Db         603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI 660

Qy         134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
Db         661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714
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Qy        188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
              | | |:  :| :|    || :       :|:|   :   || |   |    ||||||||::
Db        715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV 767

Qy        248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
              | | | : :| |: |:   ||: : | :    :    |::  ::
Db        768 CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810


RESULT 13
US-08-451-932-1
; Sequence 1, Application US/08451932
; Patent No. 5733876
;  GENERAL INFORMATION:
;    APPLICANT:  Folkman, Judah
;    APPLICANT:  O'Reilly, Michael
;    TITLE OF INVENTION:  Method of Treating an Angiogenic
;    TITLE OF INVENTION:  Disease
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303-1769
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50
;      COMPUTER:  MacIntosh
;      OPERATING SYSTEM:  7.0
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,932
;      FILING DATE:  05/26/95
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,629
;      FILING DATE:  04/26/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Larry W. Stults, Ph.D.
;      REGISTRATION NUMBER:  34,025
;      REFERENCE/DOCKET NUMBER:  05213-0123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-451-932-1

  Query Match             11.9%;  Score 369.5;  DB 1;  Length 812;
  Best Local Similarity   32.7%;  Pred. No. 9e-24;
  Matches   93;  Conservative   45;  Mismatches  107;  Indels   39;  Gaps   11;

Qy         23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRRQ 75
              |||:| : :   |        |  :  :|| : |:  |  |       |  |||| |:| :
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Qy         76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
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Db        603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI 660

Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
              |           |:|||:|: | | |    | ||| | :       |: |||   | |
Db        661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714

Qy        188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
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Db        715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV 767

Qy        248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
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Db        768 CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810


RESULT 14
US-08-452-260-1
; Sequence 1, Application US/08452260
; Patent No. 5776704
;  GENERAL INFORMATION:
;    APPLICANT:  Folkman, Judah
;    APPLICANT:  O'Reilly, Michael
;    TITLE OF INVENTION:  Method of Diagnosing an Angiogenic
;    TITLE OF INVENTION:  Disease
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303-1769
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50
;      COMPUTER:  MacIntosh
;      OPERATING SYSTEM:  7.0
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/452,260
;      FILING DATE:  05/26/95
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,629
;      FILING DATE:  04/26/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Larry W. Stults, Ph.D.
;      REGISTRATION NUMBER:  34,025
;      REFERENCE/DOCKET NUMBER:  05213-0124
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-452-260-1

  Query Match             11.9%;  Score 369.5;  DB 1;  Length 812;
  Best Local Similarity   32.7%;  Pred. No. 9e-24;
  Matches   93;  Conservative   45;  Mismatches  107;  Indels   39;  Gaps   11;

Qy         23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRRQ 75
              |||:| : :   |        |  :  :|| : |:  |  |       |  |||| |:| :
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Qy         76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
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Db        603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI 660

Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
              |           |:|||:|: | | |    | ||| | :       |: |||   | |
Db        661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714

Qy        188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
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Db        715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV 767

Qy        248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
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Db        768 CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810
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RESULT 15
US-08-326-785-1
; Sequence 1, Application US/08326785
; Patent No. 5792845
;  GENERAL INFORMATION:
;    APPLICANT:  Folkman, Judah
;    APPLICANT:  O'Reilly, Michael
;    TITLE OF INVENTION:  Angiostatin and Method of Use
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303-1769
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50
;      COMPUTER:  MacIntosh
;      OPERATING SYSTEM:  7.0
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/326,785
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/248,629
;      FILING DATE:  04/26/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Larry W. Stults, Ph.D.
;      REGISTRATION NUMBER:  34,025
;      REFERENCE/DOCKET NUMBER:  05213-0121
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-326-785-1

  Query Match             11.9%;  Score 369.5;  DB 1;  Length 812;
  Best Local Similarity   32.7%;  Pred. No. 9e-24;
  Matches   93;  Conservative   45;  Mismatches  107;  Indels   39;  Gaps   11;

Qy         23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRRQ 75
              |||:| : :   |        |  :  :|| : |:  |  |      |  |||| |:| :
Db        551 LYDYCDIPLCASA--------SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR 602

Qy         76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
                | | | |:|:|  |||||||| ||::  |   : |:||: :        :|: || |
Db        603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGLDVQEISVAKLI 660

Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
              |         |:|||:|: | | |    | ||| | :       |: |||   | |
Db        661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714

Qy        188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
              | | |:  :| :|    || :       :|:|  :   || |   |    ||||||||::
Db        715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV 767

Qy        248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
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Search completed: January  6, 2004, 10:03:44
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 6, 2004, 09:55:11 ; Search time 47 Seconds
(without alignments)
1928.359 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3108	100.0	571	20	AAY41704	Human PRO351 prote
2	3108	100.0	571	21	AAB44260	Human PRO351 (UNQ3
3	3108	100.0	571	21	AAB24046	Human PRO351 prote
4	3108	100.0	571	24	ABU61090	Human PRO351 polyp
5	2809.5	90.4	628	23	AAU82728	Amino acid sequenc
6	2809.5	90.4	628	24	ABP72375	Transmembrane seri
7	2779.5	89.4	642	24	ABP72374	Transmembrane seri
8	2304	74.1	552	23	AAE21440	Human m32404 prote
9	1454	46.8	267	21	AAY90291	Human peptidase, H
10	1436	46.2	267	22	AAB20156	Human protein SECP
11	1346	43.3	267	24	ABP72373	Transmembrane seri
12	1023	32.9	198	22	AAB20162	Human protein SECP
13	1003.5	32.3	219	21	AAY72095	Human serine prote
14	896.5	28.8	301	22	AAG67515	Amino acid sequenc
15	885	28.5	255	22	AAG67514	Amino acid sequenc
16	793	25.5	818	23	ABB98135	Human PMMM Incyte
17	793	25.5	818	23	AAU82753	Amino acid sequenc
18	724	23.3	766	22	AAM93568	Human polypeptide,
19	665.5	21.4	691	23	AAE14348	Human protease PRT
20	636.5	20.5	1128	23	AAU98890	Human protease PRT
21	636.5	20.5	1128	23	AAU82739	Amino acid sequenc
22	557.5	17.9	357	23	ABB09524	Human prostatin pr
23	556	17.9	344	23	ABB09523	Human prostatin pr
24	490	15.8	986	24	ABU12065	Human NOV12a CG922
25	476.5	15.3	1031	23	ABP60993	Novel human protei
26	450	14.5	328	22	AAM41174	Human polypeptide
27	449	14.4	272	23	ABB07286	Human prostasin-li
28	449	14.4	290	21	AAY73388	HTRM clone 3376404
29	449	14.4	290	22	AAU12282	Human PRO4327 poly
30	449	14.4	290	22	AAE03821	Human gene 4 encod
31	449	14.4	290	22	AAB73945	Human protease T.
32	449	14.4	290	23	ABG64545	Human albumin fusi
33	449	14.4	290	24	ABU66680	Human PRO polypept
34	449	14.4	290	24	ABU66956	Human secreted/tra
35	449	14.4	290	24	ABG73394	Human serine prote
36	449	14.4	290	24	ABU59761	Novel secreted and
37	449	14.4	297	19	AAW77304	Amino acid sequenc
38	448	14.4	280	23	ABG91414	Primate LP294. Ma
39	448	14.4	280	23	ABP61010	Novel human protei
40	448	14.4	282	23	ABP61011	Novel human protei
41	447.5	14.4	794	10	AAP90179	Tissue plasminogen
42	447	14.4	284	22	AAU00467	Human serine prote
43	447	14.4	316	22	AAU00468	Recombinant human
44	446	14.4	315	22	AAB73946	Fusion protein of
45	445	14.3	262	23	ABB07284	Human prostasin-li

ALIGNMENTS

RESULT 1
AAY41704
ID AAY41704 standard; Protein; 571 AA.
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AC AAY41704;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO351 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.

PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
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PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
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PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34002.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
PS Claim 12; Fig 49; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 571 AA;

Query Match 100.0%; Score 3108; DB 20; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.5e-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
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Qy 121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
Db 121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy 181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
Db 181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy 241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
Db 241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy 301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
Db 301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy 361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
Db 361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy 421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
Db 421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy 481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
Db 481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

```
Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||
Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
```

RESULT 2
AAB44260
ID AAB44260 standard; Protein; 571 AA.
XX
AC AAB44260;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO351 (UNQ308) protein sequence SEQ ID NO:132.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78486.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 12; Fig 49; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 571 AA;

Query Match 100.0%; Score 3108; DB 21; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.5e-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||
Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
```

RESULT 3
AAB24046
ID AAB24046 standard; Protein; 571 AA.
XX
AC AAB24046;
XX
DT 25-JAN-2001 (first entry)
XX
DE Human PRO351 protein sequence SEQ ID NO:12.
XX
KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
KW tumourigenesis; detection; neoplastic cell growth; proliferation;
KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
KW immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200053754-A1.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US00277.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 05-OCT-1999; 99WO-US23089.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;
PI Wood WI;
XX
DR WPI; 2000-572269/53.
DR N-PSDB; AAC58230.
XX
PT New isolated antibody for use in compositions and methods for the
PT diagnosis and treatment of neoplastic cell growth and proliferation in
PT mammals, including humans, and in monitoring tumor treatment -
XX
PS Claim 61; Fig 12; 195pp; English.
XX
CC The present invention describes an isolated antibody (Ab) that binds to
CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO538, PRO3664, PRO618,
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
CC and methods for the diagnosis and treatment of neoplastic cell growth
CC and proliferation in mammals, including humans. Genes and polypeptides
CC encoded by them, that are amplified in the genome of a tumour cell, can
CC be identified and are useful targets for the treatment and prevention of
CC certain cancers and may be used to monitor tumour treatment. Compounds
CC that inhibit the expression or activity of the identified polypeptides
CC can be identified and used as antagonists. Benign or malignant tumours,
CC inflammatory disorders and immunological disorders can be treated.
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 571 AA;

Query Match 100.0%; Score 3108; DB 21; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.5e-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||
Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
```

RESULT 4
ABU61090
ID ABU61090 standard; Protein; 571 AA.
XX
AC ABU61090;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO351 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnerary; antianaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
PN US2002169284-A1.
XX
PD 14-NOV-2002.
XX
PF 16-OCT-2001; 2001US-0978697.
XX
PR 07-OCT-1998; 98WO-US21141.
PR 20-NOV-1998; 98WO-US24855.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.

PR 22-MAR-2001; 2001WO-US09552.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 17-OCT-1997; 97US-062250P.
PR 03-NOV-1997; 97US-064249P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066364P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077641P.
PR 11-MAR-1998; 98US-077649P.
PR 12-MAR-1998; 98US-077791P.
PR 13-MAR-1998; 98US-078004P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078910P.
PR 20-MAR-1998; 98US-078936P.
PR 20-MAR-1998; 98US-078939P.
PR 25-MAR-1998; 98US-079294P.
PR 26-MAR-1998; 98US-079656P.
PR 27-MAR-1998; 98US-079663P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079689P.
PR 27-MAR-1998; 98US-079728P.
PR 27-MAR-1998; 98US-079786P.
PR 30-MAR-1998; 98US-079920P.
PR 30-MAR-1998; 98US-079923P.
PR 26-MAY-1981; 81US-0267213.
PR 17-MAR-1998; 98US-0040220.
PR 26-JUN-1998; 98US-0105413.
PR 07-OCT-1998; 98US-0168978.
PR 02-NOV-1998; 98US-0184216.
PR 06-NOV-1998; 98US-0187368.
PR 07-DEC-1998; 98US-0202054.
PR 22-DEC-1998; 98US-0218517.
PR 05-MAR-1999; 99US-0254465.
PR 10-MAR-1999; 99US-0265686.
PR 12-APR-1999; 99US-0284291.
PR 14-MAY-1999; 99US-0311832.
PR 14-MAY-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380142.
PR 08-NOV-2000; 2000US-0709238.
PR 27-NOV-2000; 2000US-0723749.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 22-MAR-2001; 2001US-0816920.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 30-JUL-2001; 2001US-0918585.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-288163/28.
DR N-PSDB; ABX92374.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies -
XX
PS Claim 12; Fig 49; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for for identifying agonists or antagonists. The
CC bioactive molecule maybe a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, for the genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC ABU61071-ABU61164 represent the human PRO polypeptides of the
CC invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html.
XX
SQ Sequence 571 AA;

Query Match 100.0%; Score 3108; DB 24; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.5e-207;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGN 60

Qy         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGL 120

Qy        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATG 180

Qy        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQG 240

Qy        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSP 300

Qy        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHC 360

Qy        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLC 420

Qy        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGM 480

Qy        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 VCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVS 540

Qy        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||
Db        541 SLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
```

RESULT 5
AAU82728

```
ID   AAU82728 standard; Protein; 628 AA.
XX
AC   AAU82728;
XX
DT   23-APR-2002  (first entry)
XX
DE   Amino acid sequence of novel human protease #27.
XX
KW   Human; protease; cancer; immune-related disorder; cardiovascular disease;
KW   neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW   nervous system disorder; sexual dysfunction; pain; mood disorder;
KW   hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW   viral infection; human immunodeficiency virus; HIV; non-viral infection;
KW   ocular disease; cytostatic; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200200860-A2.
XX
PD   03-JAN-2002.
XX
PF   26-JUN-2001; 2001WO-US20171.
XX
PR   26-JUN-2000; 2000US-214047P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman G,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Charydczak G;
XX
DR   WPI; 2002-139913/18.
DR   N-PSDB; ABK31770.
XX
PT   Nucleic acids encoding novel human proteases, useful for useful for
PT   treating diseases and disorders such as cancers, immune-related
PT   diseases and disorders, cardiovascular disease (e.g. restenosis) and
PT   inflammatory disorders -
XX
PS   Claim 6; Fig 2K; 313pp; English.
XX
CC   The present invention relates to the isolation of novel human
CC   proteases, and the nucleic acids encoding them. The sequences of
CC   the invention are useful for treating diseases and disorders such as
CC   cancers (e.g. breast, colon, lung), immune-related diseases and disorders
CC   (e.g. inflammatory diseases and asthma), cardiovascular diseases
CC   (e.g. restenosis and coronary thrombosis), brain or neuronal-associated
CC   diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory
CC   disorders (e.g. rheumatoid arthritis and psoriasis), central or
CC   peripheral nervous system diseases, migraines, pain, sexual dysfunction,
CC   mood disorders, attention disorders, cognition disorders, hypotension,
CC   hypertension, psychotic disorders, neurological disorders
CC   (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias.
CC   The nucleic acids and polypeptides are also useful for treating viral
CC   infections caused by human immunodeficiency virus (HIV), and non-viral
CC   infections such as ocular disease (e.g. glaucoma) and macular
CC   degeneration. AAU82702-AAU82760 represent the novel human proteases of
CC   the invention.
XX
SQ   Sequence   628 AA;

  Query Match           90.4%;  Score 2809.5;  DB 23;  Length 628;
  Best Local Similarity   98.5%;  Pred. No. 1.4e-186;
  Matches  516;  Conservative    1;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         49 QEPQGKAK-RHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
              |   |  | : ||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 QRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 164

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 224

Qy        168 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 284

Qy        228 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 344

Qy        288 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 404

Qy        348 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 464

Qy        408 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 524

Qy        468 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 584

Qy        528 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||||||||||||||
Db        585 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC 628


RESULT 6
ABP72375
ID   ABP72375 standard; Protein; 628 AA.
XX
AC   ABP72375;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Transmembrane serine protease 20 (MTSP20) polypeptide.
XX
KW   Human; transmembrane serine protease 20; MTSP20; enzyme;
KW   endotheliase; cytostatic; dermatological; cardiant; vulnerary;
KW   ophthalmological; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003004681-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US21208.
XX
PR   03-JUL-2001; 2001US-302939P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO;
XX
DR   WPI; 2003-239207/23.
XX
PT   New type-II membrane-type serine protease 20 polypeptides, useful for
PT   preparing a medicament for diagnosing, treating or preventing cancer,
PT   dermatological disorders, aberrant wound repairs or crest syndromes -
XX
PS   Claim 42; Page 213-215; 216pp; English.
XX
CC   The present sequence is the protein sequence of novel human type
CC   II transmembrane serine protease 20 (MTSP20), an endothelial cell
CC   transmembrane protein (endotheliase) that is expressed in oesophageal
CC   tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other
CC   cell lines as well as in certain healthy cells and tissues.  The
CC   level of MTSP20 can be diagnostic of prostate, uterine, lung,
CC   oesophagus or colon cancer, or leukaemia.  The expression and/or
CC   activation of MTSP20 on, or in the vicinity of, a cell or a
CC   bodily fluid can be a marker for breast, prostate, lung, colon and
```

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CC  other cancers.  The invention provides MTSP20 polypeptides and
CC  protease domains, zymogen and activated forms, single and multi
CC  chain forms, the nucleic acids encoding them, probes and primers,
CC  expression vectors, host cells, antibodies and transgenic animals.
CC  Nucleic acids encoding MTSP20 or its protease domain can be
CC  expressed in a host cell, and the protein used in assays to identify
CC  candidate compounds that modulate MTSP activity.  A claimed method
CC  of inhibiting tumour initiation, growth or progression or for
CC  treating a malignant or pre-malignant condition, especially of the
CC  breast, cervix, prostate, lung, ovary or colon, involves
CC  administering an inhibitor of a MTSP20 polypeptide, especially an
CC  antisense oligonucleotide, double-stranded RNA or antibody (all
CC  claimed).  These inhibitors are also used in a claimed method of
CC  treating or preventing a disease or disorder associated with
CC  undesired and/or uncontrolled angiogenesis or neovascularisation,
CC  especially undesired angiogenesis associated with solid neoplasms,
CC  vascular malformations and cardiovascular disorders (especially
CC  angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion
CC  injury, arteriovenous malformations, haemangiomatosis and vascular
CC  adhesion, dyschondroplasia with vascular hamartoma (Fafucci's
CC  syndrome), hereditary haemorrhagic telangiectasia
CC  (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome),
CC  chronic inflammatory diseases (especially diabetes mellitus,
CC  haemophiliac joints, inflammatory bowel disease, nonhealing
CC  fractures, periodontitis, psoriasis, rheumatoid arthritis, venous
CC  stasis ulcers, granulations-burns, hypertrophic scars, liver
CC  cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
CC  granuloma and systemic sclerosis), aberrant wound repairs,
CC  circulatory disorders (especially Raynaud's phenomenon), crest
CC  syndromes (especially calcinosis, oesophageal, dyomotiloty,
CC  sclerodactyly and telangiectasis), dermatological disorders
CC  (especially systemic vasculitis, scleroderma, pyoderma
CC  grangrenosum, vasculopathy, venous, arterial ulcers,
CC  Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus
CC  syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu
CC  syndrome) and ocular disorders (especially blindness caused by
CC  ocular neovascular disease, corneal graft neovascularisation,
CC  macular degeneration in the eye, neovascular glaucoma, trachoma,
CC  diabetic retinopathy, myopic degeneration, retinopathy of
CC  prematurity, retrolental ribroplasia and corneal
CC  neovascularisation).
XX
SQ   Sequence   628 AA;

  Query Match             90.4%;  Score 2809.5;  DB 24;  Length 628;
  Best Local Similarity   98.5%;  Pred. No. 1.4e-186;
  Matches  516;  Conservative    1;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         49 QEPQGKAK-RHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
              |   |  | : |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 QRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 164

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 224

Qy        168 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 284

Qy        228 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 344

Qy        288 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 404

Qy        348 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 464

Qy        408 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 524

Qy        468 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 584

Qy        528 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||||||||||||||||||
Db        585 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC 628


RESULT 7
ABP72374
ID   ABP72374 standard; Protein; 642 AA.
XX
AC   ABP72374;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Transmembrane serine protease 20 (MTSP20).
XX
KW   Human; transmembrane serine protease 20; MTSP20; enzyme;
KW   endotheliase; cytostatic; dermatological; cardiant; vulnerary;
KW   ophthalmological; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Signal_peptide
FT   Protein         25..642
FT                   /label= Mature_protein
FT   Domain          82..99
FT                   /note= "transmembrane domain"
FT   Cleavage-site   112..113
FT                   /note= "protease activation cleavage site"
FT   Domain          113..343
FT                   /note= "trypsin-like serine protease domain,
FT                         specifically described in Claim 11"
FT   Cleavage-site   375..376
FT                   /note= "protease activation cleavage site"
FT   Domain          376..624
FT                   /note= "trypsin-like serine protease domain,
FT                         specifically described in Claim 9"
FT   Region          624..642
FT                   /note= "region specifically described in Claim 5"
FT   Modified-site   77
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   621
FT                   /note= "potential N-glycosylation site"
XX
PN   WO2003004681-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US21208.
XX
PR   03-JUL-2001; 2001US-302939P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO;
XX
DR   WPI; 2003-239207/23.
DR   N-PSDB; ABZ58499.
XX
PT   New type-II membrane-type serine protease 20 polypeptides, useful for
PT   preparing a medicament for diagnosing, treating or preventing cancer,
PT   dermatological disorders, aberrant wound repairs or crest syndromes -
XX
PS   Claim 5; Page 212-213; 216pp; English.
XX
```

CC The present sequence is the protein sequence of novel human type
CC II transmembrane serine protease 20 (MTSP20), an endothelial cell
CC transmembrane protein (endotheliase) that is expressed in oesophageal
CC tumour tissues, in lung carcinoma, colon, cervix, leukaemia and other
CC cell lines as well as in certain healthy cells and tissues. The
CC level of MTSP20 can be diagnostic of prostate, uterine, lung,
CC oesophagus or colon cancer, or leukaemia. The expression and/or
CC activation of MTSP20 on, or in the vicinity of, a cell or a
CC bodily fluid can be a marker for breast, prostate, lung, colon and
CC other cancers. The invention provides MTSP20 polypeptides and
CC protease domains, zymogen and activated forms, single and multi
CC chain forms, the nucleic acids encoding them, probes and primers,
CC expression vectors, host cells, antibodies and transgenic animals.
CC Nucleic acids encoding MTSP20 or its protease domain can be
CC expressed in a host cell, and the protein used in assays to identify
CC candidate compounds that modulate MTSP activity. A claimed method
CC of inhibiting tumour initiation, growth or progression or for
CC treating a malignant or pre-malignant condition, especially of the
CC breast, cervix, prostate, lung, ovary or colon, involves
CC administering an inhibitor of a MTSP20 polypeptide, especially an
CC antisense oligonucleotide, double-stranded RNA or antibody (all
CC claimed). These inhibitors are also used in a claimed method of
CC treating or preventing a disease or disorder associated with
CC undesired and/or uncontrolled angiogenesis or neovascularisation,
CC especially undesired angiogenesis associated with solid neoplasms,
CC vascular malformations and cardiovascular disorders (especially
CC angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion
CC injury, arteriovenous malformations, haemangiomatosis and vascular
CC adhesion, dyschondroplasia with vascular hamartoma (Fafucci's
CC syndrome), hereditary haemorrhagic telangiectasia
CC (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome),
CC chronic inflammatory diseases (especially diabetes mellitus,
CC haemophiliac joints, inflammatory bowel disease, nonhealing
CC fractures, periodontitis, psoriasis, rheumatoid arthritis, venous
CC stasis ulcers, granulations-burns, hypertrophic scars, liver
CC cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
CC granuloma and systemic sclerosis), aberrant wound repairs,
CC circulatory disorders (especially Raynaud's phenomenon), crest
CC syndromes (especially calcinosis, oesophageal, dyomotiloty,
CC sclerodactyly and telangiectasis), dermatological disorders
CC (especially systemic vasculitis, scleroderma, pyoderma
CC grangrenosum, vasculopathy, venous, arterial ulcers,
CC Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus
CC syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu
CC syndrome) and ocular disorders (especially blindness caused by
CC ocular neovascular disease, corneal graft neovascularisation,
CC macular degeneration in the eye, neovascular glaucoma, trachoma,
CC diabetic retinopathy, myopic degeneration, retinopathy of
CC prematurity, retrolental ribroplasia and corneal
CC neovascularisation).
XX
SQ Sequence 642 AA;

Query Match 89.4%; Score 2779.5; DB 24; Length 642;
Best Local Similarity 98.5%; Pred. No. 1.7e-184;
Matches 511; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

```
Qy         49 QEPQGKAK-RHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
              |   |  | : ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 QRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 164

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 224

Qy        168 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 HRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 284

Qy        228 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 344

Qy        288 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 ARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGA 404

Qy        348 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 LVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLA 464

Qy        408 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 467
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 QPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHA 524

Qy        468 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 527
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 APGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPA 584

Qy        528 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANIS 566
              |||||||||||||||||||||||||||||||||||||
Db        585 VFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANIS 623
```

RESULT 8
AAE21440
ID AAE21440 standard; Protein; 552 AA.
XX
AC AAE21440;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human m32404 protein.
XX
KW Human; trypsin; m32404 protein; bone disorder; osteoporosis; osteopenia;
KW tropical sprue; immune disorder; cellular proliferative disorder; asthma;
KW psoriasis; allergy; carcinoma; leukaemia; haematopoietic disorder;
KW liver disorder; sarcoma; cardiovascular disorder; valvular disease;
KW arrhythmia; cardiomyopathy; viral disease; pain; metabolic disorder;
KW vaccine; gene therapy; protein therapy; cytostatic; immunomodulatory;
KW virucide; analgesic; enzyme.
XX
OS Homo sapiens.
XX
PN WO200226802-A2.
XX
PD 04-APR-2002.
XX
PF 24-SEP-2001; 2001WO-US29904.
XX
PR 25-SEP-2000; 2000US-235023P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers RA;
XX
DR WPI; 2002-315795/35.
DR N-PSDB; AAD33878.
XX
PT Nucleic acids encoding human trypsin m32404, useful for preventing
PT diagnosing and treating e.g. bone disorders, cellular proliferative
PT disorders and immune disorders -
XX
PS Claim 5; Page 114; 125pp; English.
XX
CC The present invention relates to human trypsin designated m32404 proteins
CC and polynucleotides encoding such proteins. m32404 sequences are useful
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate m32404 trypsin expression. They are used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of m32404 trypsin by
CC expressing inactive proteins or to supplement the patients own production
CC of m32404 trypsin. They are also used to prevent, diagnose and/or treat
CC bone disorders (e.g. osteoporosis, osteopenia, tropical sprue), immune
CC disorders (e.g. psoriasis, asthma, allergies), cellular proliferative
CC disorders (e.g. carcinoma, sarcoma and leukaemias), haematopoietic

```
CC   disorders, liver disorders, cardiovascular disorders (e.g. valvular
CC   disease, arrhythmias and cardiomyopathies), viral diseases, pain and/or
CC   metabolic disorders. Sequences of the invention are used as vaccines.
CC   They are also used in gene therapy and protein therapy. The present
CC   sequence is human m32404 protein.
XX
SQ   Sequence   552 AA;

  Query Match            74.1%;  Score 2304;  DB 23;  Length 552;
  Best Local Similarity  80.7%;  Pred. No. 1.3e-151;
  Matches  421;  Conservative   26;  Mismatches   69;  Indels    6;  Gaps    2;

Qy         50 EPQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWS 109
              |||      |||:|||||||||||||| |||||||||||||||||||| |  ||:|||
Db         37 EPQ-----EGNTLPGEWPWQASVRRQGVHICSGSLVADTWVLTAAHCFEKMATAELSSWS 91

Qy        110 VVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHR 169
              ||||||::|| ||||||||||||||:|||||||||||||||| |||  | |||||| :
Db         92 VVLGSLKQEGQSPGAEEVGVAALQLPKAYNHYSQGSDLALLQLTHPTVQTTLCLPQPTYH 151

Qy        170 FPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGG 229
              ||||||||||||||:|||   ||||||||||||||||:||:|||| ||||||||||||
Db        152 FPFGASCWATGWDQNTSDVSRTLRNLRLRLISRPTCNCLYNRLHQRLLSNPARPGMLCGG 211

Qy        230 PQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQAR 289
              ||| |||||||||||:| |||||||| ||||| | ||||| |||||: | |||||||
Db        212 AQPGEQGPCQGDSGGPVMCREPDGHWVQVGIISFTSKCAQEDTPVLLTDMAVHSSWLQAH 271

Qy        290 VQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALV 349
              |  |||| |:|   :||||:|||||||||:||||||| | |||:||| | |:||||||||
Db        272 VHEAAFLVQAPGVVKMSDENSCVACGSLRSAGPQAGALSQWPWDARLKHHGKLACGGALV 331

Qy        350 SEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQP 409
              ||  |||||||||||  ||||||||  |||||||||||||||||||||:| ||||||
Db        332 SEVVVLTAAHCFIGRQTLEEWSVGLGAGPEEWGLKQLILHGAYTHPEGGYDVAFLLLAQP 391

Qy        410 VTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAP 469
              ||||  |||||||| |||||||| |||||  :  |||:  ||||||:||| |||| ||||
Db        392 VTLGPGLRPLCLPYADHHLPDGEHGWVLGLTQK-AGINYPQTVPVTVLGPMACSRQHAAP 450

Qy        470 GGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVF 529
              || | |||||||||: ||| | |||||||||||||:|||||| ||||||| ||  |:|||
Db        451 GGTGIPILPGMVCTTVVGEPPHCEGLSGAPLVHEIRGTWFLVGLHSFGDTCQSSAKPAVF 510

Qy        530 TALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQPTSC 571
              || |||||:|:|||||||||||||| |||| | ||| ||
Db        511 AALSAYEDWISNLDWQVYFAEEPEPEAETGSCLVNSSQPASC 552


RESULT 9
AAY90291
ID   AAY90291 standard; Protein; 267 AA.
XX
AC   AAY90291;
XX
DT   24-OCT-2000  (first entry)
XX
DE   Human peptidase, HPEP-8 protein sequence.
XX
KW   Human; peptidase; cell proliferative disorder; arteriosclerosis;
KW   psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;
KW   inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;
KW   Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;
KW   metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;
KW   glycogen storage disease; obesity; therapy; HPEP-8.
XX
OS   Homo sapiens.
XX
PN   WO200042201-A2.
XX
PD   20-JUL-2000.
XX
PF   11-JAN-2000; 2000WO-US00641.
XX
PR   11-JAN-1999;   99US-0172247.
PR   03-MAY-1999;   99US-0132253.
PR   27-MAY-1999;   99US-0136653.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O,  Hillman JL,  Tang YT,  Azimzai Y,  Baughn MR,  Lal P;
PI   Yue H,  Lu DAM;
XX
DR   WPI; 2000-482832/42.
DR   N-PSDB; AAA37664.
XX
PT   An isolated polypeptide for diagnosis, prevention  and treatment of
PT   cell proliferative, autoimmune/ inflammatory and metabolic disorders
PT   comprises a sequence encoding a human peptidase -
XX
PS   Claim 2; Page 99; 131pp; English.
XX
CC   This sequence represents a human peptidase, designated HPEP-8. The
CC   invention relates to 18 human peptidases designated HPEP-1 to HPEP-18,
CC   respectively. The peptidases can be used for treating a disease or
CC   condition associated with decreased expression or over expression of
CC   functional human peptidases. The diseases that can be diagnosed,
CC   prevented and treated include cell proliferative disorders (such as
CC   arteriosclerosis, psoriasis, myelofibrosis, and cancers),
CC   autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies,
CC   Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple
CC   sclerosis, and scleroderma), infections, and metabolic disorders (such as
CC   Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases
CC   and obesity).
XX
SQ   Sequence   267 AA;

  Query Match            46.8%;  Score 1454;  DB 21;  Length 267;
  Best Local Similarity  99.6%;  Pred. No. 4.8e-93;
  Matches  266;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        305 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR 60

Qy        365 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYP 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA 120

Qy        425 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 180

Qy        485 AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 240

Qy        545 QVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||
Db        241 QVYFAEEPEPEAEPGSCLANISQPTSC 267


RESULT 10
AAB20156
ID   AAB20156 standard; Protein; 267 AA.
XX
AC   AAB20156;
XX
DT   30-APR-2001  (first entry)
XX
DE   Human protein SECP2.
XX
KW   SECP2; secreted protein; human; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
```

```
PN   WO200105971-A2.
XX
PD   25-JAN-2001.
XX
PF   20-JUL-2000; 2000WO-US19890.
XX
PR   20-JUL-1999;   99US-0144722.
PR   29-NOV-1999;   99US-0167785.
PR   19-JUL-2000; 2000US-0619252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Fernandes E;
XX
DR   WPI; 2001-091973/10.
DR   N-PSDB; AAF30189.
XX
PT   New polypeptide designated SECP, its encoding nucleic acid and its
PT   immunospecific antibody, useful for diagnosing, preventing and treating
PT   SECP-associated disorders such as cancer -
XX
PS   Claim 1; Fig 2; 124pp; English.
XX
CC   The present sequence is that of novel human protein SECP2,
CC   which is predicted to localise in the microbody (peroxisome),
CC   and which does not appear to include a signal peptide.  The
CC   protein shows homology to human PRO351 protein, and to a region
CC   of human prostatin precursor.  The invention provides 9 novel
CC   SECP proteins (see AAB20155-63), nucleic acids encoding them
CC   (see AAF30188-96), antibodies, mutants or fragments.  These can
CC   be used to detect, treat or prevent an SECP-associated disorder,
CC   to screen for predisposition to such a disorder, and to identify
CC   agents that modulate the expression or activity of SECP.
XX
SQ   Sequence   267 AA;

  Query Match             46.2%;  Score 1436;  DB 22;  Length 267;
  Best Local Similarity   98.9%;  Pred. No. 8.4e-92;
  Matches  264;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        305 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFNGR 60

Qy        365 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYP 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db         61 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRALCLPYF 120

Qy        425 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 180

Qy        485 AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW 240

Qy        545 QVYFAEEPEPEAEPGSCLANISQPTSC 571
              |||||||||||||||||||||||||||
Db        241 QVYFAEEPEPEAEPGSCLANISQPTSC 267


RESULT 11
ABP72373
ID   ABP72373 standard; Protein; 267 AA.
XX
AC   ABP72373;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Transmembrane serine protease 20 (MTSP20) protease domain.
XX
KW   Human; transmembrane serine protease 20; MTSP20; enzyme;
KW   endotheliase; cytostatic; dermatological; cardiant; vulnerary;
KW   ophthalmological; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003004681-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US21208.
XX
PR   03-JUL-2001; 2001US-302939P.
XX
PA   (CORV-) CORVAS INT INC.
XX
PI   Madison EL,  Ong EO;
XX
DR   WPI; 2003-239207/23.
DR   N-PSDB; ABZ58498.
XX
PT   New type-II membrane-type serine protease 20 polypeptides, useful for
PT   preparing a medicament for diagnosing, treating or preventing cancer,
PT   dermatological disorders, aberrant wound repairs or crest syndromes -
XX
PS   Claim 5; Page 204-205; 216pp; English.
XX
CC   The present sequence is the protein sequence of protease domain 2
CC   of novel human type II transmembrane serine protease 20 (MTSP20).
CC   MTSP20 (see also ABP72374) is an endothelial cell transmembrane
CC   protein (endotheliase) that is expressed in oesophageal tumour
CC   tissues, in lung carcinoma, colon, cervix, leukaemia and other
CC   cell lines as well as in certain healthy cells and tissues.  The
CC   level of MTSP20 can be diagnostic of prostate, uterine, lung,
CC   oesophagus or colon cancer, or leukaemia.  The expression and/or
CC   activation of MTSP20 on, or in the vicinity of, a cell or a
CC   bodily fluid can be a marker for breast, prostate, lung, colon and
CC   other cancers.  The invention provides MTSP20 polypeptides and
CC   protease domains, zymogen and activated forms, single and multi
CC   chain forms, the nucleic acids encoding them, probes and primers,
CC   expression vectors, host cells, antibodies and transgenic animals.
CC   Nucleic acids encoding MTSP20 or its protease domain can be
CC   expressed in a host cell, and the protein used in assays to identify
CC   candidate compounds that modulate MTSP activity.  A claimed method
CC   of inhibiting tumour initiation, growth or progression or for
CC   treating a malignant or pre-malignant condition, especially of the
CC   breast, cervix, prostate, lung, ovary or colon, involves
CC   administering an inhibitor of a MTSP20 polypeptide, especially an
CC   antisense oligonucleotide, double-stranded RNA or antibody (all
CC   claimed).  These inhibitors are also used in a claimed method of
CC   treating or preventing a disease or disorder associated with
CC   undesired and/or uncontrolled angiogenesis or neovascularisation,
CC   especially undesired angiogenesis associated with solid neoplasms,
CC   vascular malformations and cardiovascular disorders (especially
CC   angiofibroma, angiolipoma, atherosclerosis, restenosis/reperfusion
CC   injury, arteriovenous malformations, haemangiomatosis and vascular
CC   adhesion, dyschondroplasia with vascular hamartoma (Fafucci's
CC   syndrome), hereditary haemorrhagic telangiectasia
CC   (Rendu-Osler-Weber syndrome) and von Hipple Lindau syndrome),
CC   chronic inflammatory diseases (especially diabetes mellitus,
CC   haemophiliac joints, inflammatory bowel disease, nonhealing
CC   fractures, periodontitis, psoriasis, rheumatoid arthritis, venous
CC   stasis ulcers, granulations-burns, hypertrophic scars, liver
CC   cirrhosis, osteoradionecrosis, postoperative adhesions, pyogenic
CC   granuloma and systemic sclerosis), aberrant wound repairs,
CC   circulatory disorders (especially Raynaud's phenomenon), crest
CC   syndromes (especially calcinosis, oesophageal, dyomotiloty,
CC   sclerodactyly and telangiectasis), dermatological disorders
CC   (especially systemic vasculitis, scleroderma, pyoderma
CC   grangrenosum, vasculopathy, venous, arterial ulcers,
CC   Sturge-Weber syndrome, Post-wine stains, blue rubber bleb naevus
CC   syndrome, Klippel-Trenaunay-Weber syndrome and Osler-Weber-Rendu
CC   syndrome) and ocular disorders (especially blindness caused by
CC   ocular neovascular disease, corneal graft neovascularisation,
CC   macular degeneration in the eye, neovascular glaucoma, trachoma,
```

```
CC   diabetic retinopathy, myopic degeneration, retinopathy of
CC   prematurity, retrolental ribroplasia and corneal
CC   neovascularisation).
XX
SQ   Sequence   267 AA;

  Query Match            43.3%;  Score 1346;  DB 24;  Length 267;
  Best Local Similarity   98.8%;  Pred. No. 1.5e-85;
  Matches  245;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        319 TAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRP 378
              ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db          1 TAGPQAGAPSPWPWEARLMHQGQLACGGALVSEETVLTVAHCFIGRQAPEEWSVGLGTRP 60

Qy        379 EEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERGWVLG 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERGWVLG 120

Qy        439 RARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLSGA 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLSGA 180

Qy        499 PLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP 240

Qy        559 GSCLANIS 566
              |||||:|
Db        241 GSCLANMS 248


RESULT 12
AAB20162
ID   AAB20162 standard; Protein; 198 AA.
XX
AC   AAB20162;
XX
DT   30-APR-2001  (first entry)
XX
DE   Human protein SECP8.
XX
KW   SECP8; secreted protein; human; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO200105971-A2.
XX
PD   25-JAN-2001.
XX
PF   20-JUL-2000; 2000WO-US19890.
XX
PR   20-JUL-1999;   99US-0144722.
PR   29-NOV-1999;   99US-0167785.
PR   19-JUL-2000; 2000US-0619252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Fernandes E;
XX
DR   WPI; 2001-091973/10.
DR   N-PSDB; AAF30195.
XX
PT   New polypeptide designated SECP, its encoding nucleic acid and its
PT   immunospecific antibody, useful for diagnosing, preventing and treating
PT   SECP-associated disorders such as cancer -
XX
PS   Claim 1; Fig 8; 124pp; English.
XX
CC   The present sequence is that of novel human protein SECP8,
CC   which is predicted to localise in the cytoplasm, and which does
CC   not appear to include a signal peptide.  The invention provides 9
CC   novel SECP proteins (see AAB20155-63), nucleic acids encoding them
CC   (see AAF30188-96), antibodies, mutants or fragments.  These can
CC   be used to detect, treat or prevent an SECP-associated disorder,
CC   to screen for predisposition to such a disorder, and to identify
CC   agents that modulate the expression or activity of SECP.
XX
SQ   Sequence   198 AA;

  Query Match            32.9%;  Score 1023;  DB 22;  Length 198;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-63;
  Matches  188;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        305 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR 60

Qy        365 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYP 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA 120

Qy        425 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS 180

Qy        485 AVGELPSCE 493
              |||||||||
Db        181 AVGELPSCE 189


RESULT 13
AAY72095
ID   AAY72095 standard; Protein; 219 AA.
XX
AC   AAY72095;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Human serine protease #6 encoded by clone HTTJK57.
XX
KW   Human; serine protease; osteopathic; immunosuppressive; antiallergic;
KW   antiinflammatory; cytostatic; cardiant; neuroprotective; nootropic;
KW   neuroleptic; vulnerary; opthalmological; antibacterial; antiviral;
KW   antifungal; antiparasitic; gene therapy; diagnosis; prevention; glaucoma;
KW   treatment; bone formation disorder; osteoporosis; arthritis; cancer;
KW   connective tissue disorder; autoimmune disorder; wound healing; asthma;
KW   systemic lupus erythematosus; male reproductive system disorder;
KW   testicular cancer; digestion and food absorption disorder; arrhythmia;
KW   Crohn's disease; neurodegenerative disease; Alzheimer's disease; allergy;
KW   behavioral disorder; Tourette's syndrome; acute myelogenous leukaemia;
KW   cardiovascular disorder; occular disorder; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          24..39
FT                   /note= "Immunogenic epitope"
FT   Domain          70..75
FT                   /label= Histidine_active_site_domain
FT   Region          115..123
FT                   /note= "Immunogenic epitope"
FT   Region          158..167
FT                   /note= "Immunogenic epitope"
FT   Region          190..202
FT                   /note= "Immunogenic epitope"
XX
PN   WO200068247-A2.
XX
PD   16-NOV-2000.
XX
PF   05-MAY-2000; 2000WO-US12207.
XX
PR   07-MAY-1999;   99US-0133239.
PR   20-MAY-1999;   99US-0135163.
PR   03-AUG-1999;   99US-0147005.
PR   09-SEP-1999;   99US-0152935.
```

```
PR   01-NOV-1999;   99US-0162979.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Shi Y,  Young PE,  Ni J;
XX
DR   WPI; 2000-679799/66.
DR   N-PSDB; AAD02325.
XX
PT   New nucleic acid molecules encoding human serine protease polypeptides,
PT   useful for diagnosis, prevention and/or treatment of disorders e.g.
PT   osteoporosis, lupus erythematosus and Alzheimer's -
XX
PS   Claim 12; Page 282-283; 289pp; English.
XX
CC   The present sequence is human serine protease #6 from clone
CC   HTTJK57 (ATCC Deposit No: PTA538).
CC   The invention relates to human serine proteases and their cDNA clones.
CC   It is used in methods for the diagnosis, prevention and treatment of
CC   various disorders related to serine protease such as bone formation
CC   disorders (osteoporosis), connective tissue disorders (arthritis),
CC   autoimmune disorders (systemic lupus erythematosus), wound healing, male
CC   reproductive system disorders (testicular cancer), digestion and food
CC   absorption disorders (Crohn's disease), neurodegenerative diseases
CC   (Alzheimer's disease), behavioral disorders (Tourette's syndrome),
CC   proliferative and cancerous conditions (acute myelogenous leukaemia),
CC   allergic reactions (asthma), cardiovascular disorders (arrhythmia),
CC   occular disorders (glaucoma) and infectious diseases caused by bacteria,
CC   viruses, fungi or parasites. It is also useful for screening therapeutic
CC   compounds. Serine proteases are used as immunological probes or
CC   polymorphic markers for the identification of chromosomes, cells and
CC   tissues in biological samples, identification of male contraceptive
CC   agents, delivery of compositions to targetted cells expressing a
CC   receptor for serine protease, hybridisation probes and molecular weight
CC   markers. Serine protease nucleic acids are also useful in gene therapy.
CC   Note: The present sequence shown in page 282-283 of sequence listing has
CC   been assigned SEQ ID NO: 16. But the sequence, peptide fragment #14
CC   related to human serine protease (AAY72117) shown in page 15 is also
CC   referred as SEQ ID NO: 16.
XX
SQ   Sequence   219 AA;

  Query Match             32.3%;  Score 1003.5;  DB 21;  Length 219;
  Best Local Similarity   95.8%;  Pred. No. 6.5e-62;
  Matches  184;  Conservative    1;  Mismatches    6;  Indels    1;  Gaps    1;

Qy         49 QEPQGKAK-RHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
              |   |  | : |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         27 QRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 86

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 167
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPA 146

Qy        168 HRFPPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 HRFPPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLC 206

Qy        228 GGPQPGVQGPCQ 239
              ||||||||||||
Db        207 GGPQPGVQGPCQ 218


RESULT 14
AAG67515
ID   AAG67515 standard; Protein; 301 AA.
XX
AC   AAG67515;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Amino acid sequence of a human secreted polypeptide.
XX
KW   Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW   gastrointestinal ulceration; spinal cord disease; trachea disease;
KW   thyroid gland disease; ovary disease; prostate disease; heart disease;
KW   renal gland disease; small intestine disease; thymus disease;
KW   lymph node disease; muscular system disease; colon disease;
KW   lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW   myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW   microbial disease; immune disorder; inflammation; transplant rejection;
KW   bone thickness; bone density; ferroxidase loss; apoptosis;
KW   vascular smooth cell proliferation; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200166690-A2.
XX
PD   13-SEP-2001.
XX
PF   05-MAR-2001; 2001WO-US07143.
XX
PR   06-MAR-2000; 2000US-0187107.
PR   13-MAR-2000; 2000US-0188916.
PR   03-OCT-2000; 2000US-0236874.
PR   03-OCT-2000; 2000US-0237846.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2001-570768/64.
DR   N-PSDB; AAH78207.
XX
PT   Novel isolated secreted polypeptide useful for treating nervous and
PT   muscular diseases, gastrointestinal ulceration, coagulation and immune
PT   disorders, microbial diseases, inflammation and transplant rejection -
XX
PS   Claim 1; Page 74-75; 102pp; English.
XX
CC   The present sequence represents a human secreted polypeptide. The
CC   secreted polypeptides and polynucleotides are useful for treating
CC   nervous and muscular diseases, for inhibiting tumour formation and
CC   metastasis, for treating gastrointestinal ulceration, for preventing
CC   and treating diseases in spinal cord, thyroid gland, ovary, prostate,
CC   renal gland, small intestine, heart, trachea, thymus, lymph node,
CC   muscular system and colon, for treating lipase deficiency in cystic
CC   fibrosis and pancreatitis, for treating undesirable clot formation
CC   such as myocardial infarction, during angioplasty and all surgical
CC   procedures that require decreased blood clot formation, for treating
CC   liver diseases, coagulation disorders and microbial diseases, for
CC   treating immune disorders, for treating inflammation and transplant
CC   rejection, for enhancing bone thickness and increasing bone density,
CC   for reducing the loss of essential ferroxidases, for suppressing
CC   apoptosis, and for regulating vascular smooth cell proliferation. They
CC   may also be used as vaccines.
XX
SQ   Sequence   301 AA;

  Query Match             28.8%;  Score 896.5;  DB 22;  Length 301;
  Best Local Similarity   38.3%;  Pred. No. 2.4e-54;
  Matches  199;  Conservative   10;  Mismatches   44;  Indels  267;  Gaps    6;

Qy         53 GKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCF-EKAAATELNSWSVV 111
              ||| |     || |||:| |   |:  | |:||:::|||  | || |:   |
Db         24 GKAPR-----PGAWPWEAQVMVPGSRPCHGALVSESWVLAPASCFLEQVTHTLCCCRMTR 78

Qy        112 LGSLQREGLSPG---AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAH 168
              :|:       ||      |    |: ||||||||||||||||||||||||||||||||||
Db         79 VGAFCARRRGPGFWLESETFPVAVYLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAH 138

Qy        169 RFPPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 RFPPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG 198
```

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Qy        229 GPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQA 288
              ||||||||||
Db        199 GPQPGVQGPCQ---------------------------------------------------- 209

Qy        289 RVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGAL 348

Db        210 ------------------------------------------------------------ 209

Qy        349 VSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQ 408

Db        210 ------------------------------------------------------------ 209

Qy        409 PVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAA 468

Db        210 ------------------------------------------------------------ 209

Qy        469 PGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAV 528
                                  || |||||||||||||||||||||||||||||||
Db        210 ------------------------GLFGAPLVHEVRGTWFLAGLHSFGDACQGPARPAV 244

Qy        529 FTALPAYEDWVSSLDW--QVYFAEEPEPEAEPGSCLANIS 566
              ||||||      |  |  ||||||||||||||||||||
Db        245 FTALPAMR--TGSAVWTRQVYFAEEPEPEAEPGSCLANIS 282
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RESULT 15
AAG67514
ID   AAG67514 standard; Protein; 255 AA.
XX
AC   AAG67514;
XX
DT   26-NOV-2001  (first entry)
XX
DE   Amino acid sequence of a human secreted polypeptide.
XX
KW   Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW   gastrointestinal ulceration; spinal cord disease; trachea disease;
KW   thyroid gland disease; ovary disease; prostate disease; heart disease;
KW   renal gland disease; small intestine disease; thymus disease;
KW   lymph node disease; muscular system disease; colon disease;
KW   lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW   myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW   microbial disease; immune disorder; inflammation; transplant rejection;
KW   bone thickness; bone density; ferroxidase loss; apoptosis;
KW   vascular smooth cell proliferation; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200166690-A2.
XX
PD   13-SEP-2001.
XX
PF   05-MAR-2001; 2001WO-US07143.
XX
PR   06-MAR-2000; 2000US-0187107.
PR   13-MAR-2000; 2000US-0188916.
PR   03-OCT-2000; 2000US-0236874.
PR   03-OCT-2000; 2000US-0237846.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z;
XX
DR   WPI; 2001-570768/64.
DR   N-PSDB; AAH78206.
XX
PT   Novel isolated secreted polypeptide useful for treating nervous and
PT   muscular diseases, gastrointestinal ulceration, coagulation and immune
PT   disorders, microbial diseases, inflammation and transplant rejection -
XX
PS   Claim 1; Page 73-74; 102pp; English.
XX
```

```
CC   The present sequence represents a human secreted polypeptide. The
CC   secreted polypeptides and polynucleotides are useful for treating
CC   nervous and muscular diseases, for inhibiting tumour formation and
CC   metastasis, for treating gastrointestinal ulceration, for preventing
CC   and treating diseases in spinal cord, thyroid gland, ovary, prostate,
CC   renal gland, small intestine, heart, trachea, thymus, lymph node,
CC   muscular system and colon, for treating lipase deficiency in cystic
CC   fibrosis and pancreatitis, for treating undesirable clot formation
CC   such as myocardial infarction, during angioplasty and all surgical
CC   procedures that require decreased blood clot formation, for treating
CC   liver diseases, coagulation disorders and microbial diseases, for
CC   treating immune disorders, for treating inflammation and transplant
CC   rejection, for enhancing bone thickness and increasing bone density,
CC   for reducing the loss of essential ferroxidases, for suppressing
CC   apoptosis, and for regulating vascular smooth cell proliferation. They
CC   may also be used as vaccines.
XX
SQ   Sequence   255 AA;
```

```
  Query Match             28.5%;  Score 885;  DB 22;  Length 255;
  Best Local Similarity   37.8%;  Pred. No. 1.2e-53;
  Matches  196;  Conservative    5;  Mismatches   30;  Indels  288;  Gaps    7;

Qy         60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
              |  || |||| |:   | ||| |||:| :|||:|||||                  |:
Db          6 NAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTG----------------RQY 49

Qy        120 LSPGAEEVGVAALQLP-----RAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGA 174
                |       |   ||     ||||||||||||||||||||||||||||||||||||||
Db         50 RCPETRRTRSA---LPTRKRRRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGA 106

Qy        175 SCWATGWDQDTSD------APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG 228
              ||||||||||||      |||||||||||||||||||||||||||||||||||||||||
Db        107 SCWATGWDQDTSDAPSLSPAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCG 166

Qy        229 GPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQA 288
              ||||||||||
Db        167 GPQPGVQGPCQ---------------------------------------------------- 177

Qy        289 RVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGAL 348

Db        178 ------------------------------------------------------------ 177

Qy        349 VSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQ 408

Db        178 ------------------------------------------------------------ 177

Qy        409 PVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAA 468

Db        178 ------------------------------------------------------------ 177

Qy        469 PGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAV 528
                                  || |||||||||||||||||||||||||||||||
Db        178 ------------------------GLFGAPLVHEVRGTWFLAGLHSFGDACQGPARPAV 212

Qy        529 FTALPAYEDWVSSLDW--QVYFAEEPEPEAEPGSCLANI 565
              ||||||      |  |  |||||||||||||||||||
Db        213 FTALPAMR--TGSAVWTRQVYFAEEPEPEAEPGSCLANI 249
```

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Search completed: January  6, 2004, 10:01:15
Job time : 49 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 6, 2004, 09:55:46 ; Search time 17 Seconds
(without alignments)
1579.544 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	449	14.4	290	1	MPN_HUMAN	Q9bqr3 homo sapien
2	437.5	14.1	343	1	PSS8_HUMAN	Q16651 homo sapien
3	422	13.6	342	1	PSS8_RAT	Q9es87 rattus norv
4	417	13.4	306	1	BSS4_MOUSE	Q9er10 mus musculu
5	414	13.3	342	1	PSS8_MOUSE	Q9esd1 mus musculu
6	400	12.9	317	1	BSS4_HUMAN	Q9gzn4 homo sapien
7	382	12.3	321	1	TRYG_HUMAN	Q9nrr2 homo sapien
8	371.5	12.0	812	1	PLMN_MOUSE	P20918 mus musculu
9	370.5	11.9	790	1	PLMN_PIG	P06867 sus scrofa
10	368.5	11.9	324	1	TEST_MOUSE	Q9jhj7 mus musculu
11	368.5	11.9	855	1	ST14_MOUSE	P56677 mus musculu
12	363	11.7	311	1	TRYG_MOUSE	Q9qul7 mus musculu
13	361.5	11.6	855	1	ST14_HUMAN	Q9y5y6 homo sapien
14	359.5	11.6	810	1	PLMN_HUMAN	P00747 homo sapien
15	359	11.6	454	1	TMS3_HUMAN	P57727 homo sapien
16	359	11.6	810	1	PLMN_ERIEU	Q29485 erinaceus e
17	356.5	11.5	457	1	TMS5_HUMAN	Q9h3s3 homo sapien
18	356.5	11.5	812	1	PLMN_BOVIN	P06868 bos taurus
19	355.5	11.4	338	1	PLMN_HORSE	P80010 equus cabal
20	354	11.4	422	1	DES1_HUMAN	Q9ul52 homo sapien
21	353.5	11.4	333	1	PLMN_CANFA	P80009 canis famil
22	353	11.4	417	1	HEPS_HUMAN	P05981 homo sapien
23	351.5	11.3	810	1	PLMN_MACMU	P12545 macaca mula
24	348.5	11.2	453	1	TMS3_MOUSE	Q8k1t0 mus musculu
25	347.5	11.2	455	1	TMS5_MOUSE	Q9er04 mus musculu
26	345.5	11.1	490	1	TMS2_MOUSE	Q9jiq8 mus musculu
27	344	11.1	314	1	TEST_HUMAN	Q9y6m0 homo sapien
28	342	11.0	4548	1	APOA_HUMAN	P08519 homo sapien
29	339	10.9	1420	1	APOA_MACMU	P14417 macaca mula
30	338	10.9	343	1	PLMN_SHEEP	P81286 ovis aries
31	337.5	10.9	638	1	KAL_HUMAN	P03952 homo sapien
32	336	10.8	270	1	TRYT_MERUN	P50342 meriones un
33	335	10.8	275	1	TRYT_CANFA	P15944 canis famil
34	335	10.8	436	1	HEPS_MOUSE	O35453 mus musculu
35	333	10.7	276	1	MCT6_MOUSE	P21845 mus musculu
36	330.5	10.6	273	1	MCT7_MOUSE	Q02844 mus musculu
37	330	10.6	271	1	EL2_MOUSE	P05208 mus musculu
38	330	10.6	275	1	TRYT_PIG	Q9n2d1 sus scrofa
39	329	10.6	275	1	TRB1_HUMAN	Q15661 homo sapien
40	329	10.6	275	1	TRB2_HUMAN	P20231 homo sapien
41	329	10.6	492	1	TMS2_HUMAN	O15393 homo sapien
42	328.5	10.6	274	1	MCT6_RAT	P50343 rattus norv
43	326.5	10.5	418	1	HATT_HUMAN	O60235 homo sapien
44	326.5	10.5	625	1	FA11_HUMAN	P03951 homo sapien
45	326.5	10.5	638	1	KAL_MOUSE	P26262 mus musculu

ALIGNMENTS

RESULT 1
MPN_HUMAN
ID MPN_HUMAN STANDARD; PRT; 290 AA.
AC Q9BQR3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marapsin precursor (EC 3.4.21.-).
GN MPN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.;
RT "Cloning, sequencing and expression of marapsin, a human serine
RT proteinase.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC ---

CC ---
DR EMBL; AJ306593; CAC35467.1; -.
DR HSSP; P00734; 1UVS.
DR MEROPS; S01.074; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.

FT	SIGNAL	1 22	POTENTIAL.
FT	PROPEP	23 34	POTENTIAL.
FT	CHAIN	35 290	MARAPSIN.
FT	DOMAIN	35 277	SERINE PROTEASE.
FT	ACT_SITE	75 75	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	124 124	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	229 229	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	60 76	BY SIMILARITY.
FT	DISULFID	158 235	BY SIMILARITY.
FT	DISULFID	191 214	BY SIMILARITY.
FT	DISULFID	225 253	BY SIMILARITY.
FT	CARBOHYD	55 55	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	79 79	N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 290 AA; 31940 MW; 67BDC93EC70BFF7B CRC64;

```
  Query Match             14.4%;  Score 449;  DB 1;  Length 290;
  Best Local Similarity   37.1%;  Pred. No. 4.6e-23;
  Matches   89;  Conservative   44;  Mismatches   87;  Indels   20;  Gaps    6;

Qy         60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
              :|  |||||| |::| |:| | |||:|: |||||||||   : | |  : |:||: |
Db         40 DTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCFRNTSETSL--YQVLLGARQLVQ 97

Qy        120 LSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
                | |    |  ::    |   :  :|:||::|  |   |    |:||| |:  |  | :
Db         98 PGPHAMYARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPDPSVIFETGMN 157

Qy        176 CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQ-----LHQRHLSNPARPGML 226
              || |||    ::|    |  |: | : :|  | || :|::       : : |     ||
Db        158 CWVTGWGSPSEEDLLPEPRILQKLAVPIIDTPKCNLLYSKDTEFGYQPKTIKN----DML 213

Qy        227 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
              | | : | :  |:||||||::||     |:|||:||:   ||::: | :     || :|:
Db        214 CAGFEEGKKDACKGDSGGPLVCLVGQS-WLQAGVISWGEGCARQNRPGVYIRVTAHHNWI 272


RESULT 2
PSS8_HUMAN
ID   PSS8_HUMAN     STANDARD;      PRT;   343 AA.
AC   Q16651; Q9UCA3;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Prostasin precursor (EC 3.4.21.-).
GN   PRSS8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Prostate;
RX   MEDLINE=95286644; PubMed=7768952;
RA   Yu J.X., Chao L., Chao J.;
RT   "Molecular cloning, tissue-specific expression, and cellular
RT   localization of human prostasin mRNA.";
RL   J. Biol. Chem. 270:13483-13489(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE OF 45-64.
RC   TISSUE=Semen;
RX   MEDLINE=94308140; PubMed=8034638;
RA   Yu J.X., Chao L., Chao J.;
RT   "Prostasin is a novel human serine proteinase from seminal fluid.
RT   Purification, tissue distribution, and localization in prostate
RT   gland.";
RL   J. Biol. Chem. 269:18843-18848(1994).
CC   -!- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY.
CC   -!- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A
CC       DISULFIDE BOND.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
CC       ITS C-TERMINUS.
CC   -!- TISSUE SPECIFICITY: FOUND IN PROSTATE, LIVER, SALIVARY GLAND,
CC       KIDNEY, LUNG, PANCREAS, COLON, BRONCHUS AND RENAL PROXIMAL TUBULAR
CC       CELLS. IN THE PROSTATE GLAND IT MAY BE SYNTHESIZED IN EPITHELIAL
CC       CELLS, SECRETED INTO THE DUCTS, AND EXCRETED INTO THE SEMINAL
CC       FLUID.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L41351; AAC41759.1; -.
DR   EMBL; U33446; AAB19071.1; -.
DR   EMBL; BC001462; AAH01462.1; -.
DR   PIR; A57014; A57014.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.159; -.
DR   Genew; HGNC:9491; PRSS8.
DR   MIM; 600823; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL       1     29       POTENTIAL.
FT   PROPEP      30     32       ACTIVATION PEPTIDE.
FT   CHAIN       33     44       PROSTATIN LIGHT CHAIN.
FT   CHAIN       45    322       PROSTATIN HEAVY CHAIN.
FT   PROPEP     323    343
FT   TRANSMEM   320    340       POTENTIAL.
FT   DOMAIN      45    286       SERINE PROTEASE.
FT   DISULFID    37    154       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    70     86       BY SIMILARITY.
FT   DISULFID   168    244       BY SIMILARITY.
FT   DISULFID   201    223       BY SIMILARITY.
FT   DISULFID   234    262       BY SIMILARITY.
FT   ACT_SITE    85     85       CHARGE RELAY SYSTEM.
FT   ACT_SITE   134    134       CHARGE RELAY SYSTEM.
FT   ACT_SITE   238    238       CHARGE RELAY SYSTEM.
FT   CARBOHYD   159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   343 AA;  36431 MW;  98DD6447F5A8C1B2 CRC64;

  Query Match             14.1%;  Score 437.5;  DB 1;  Length 343;
  Best Local Similarity   35.3%;  Pred. No. 3.2e-22;
  Matches  110;  Conservative   48;  Mismatches  109;  Indels   45;  Gaps   14;

Qy         51 PQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSV 110
              || :     : | |:|||| |:  :| |:| ||||:: |||:|||||      |  :: |
Db         41 PQARITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE--AYEV 98

Qy        111 VLGSLQREGLSPGAEEVGVAALQ--LPRAYNHYSQGS--DLALLQLAHPTTHT----PLC 162
               ||: | :  |   |:  |: |:  :|   ::  :||  |:|||||: | | :    |:|
Db         99 KLGAHQLDSYS---EDAKVSTLKDIIPHP-SYLQEGSQGDIALLQLSRPITFSRYIRPIC 154

Qy        163 LPQPAHRFPFGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQRHLS 218
```

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              ||     || |  |  |||           |  |: | : |||| ||||:||   :
Db        155 LPAANASFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEP 214

Qy        219 NPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTN 278
              :  :  |:| |   | :  ||||||||: |   :| |   ||:|:  :|   : | : |
Db        215 HFVQEDMVCAGYVEGGKDACQGDSGGPLSC-PVEGLWYLTGIVSWGDACGARNRPGVYTL 273

Qy        279 TAAHSSWLQARV---QGAAFLAQSPETPEMSDEDSCVACGS------------LR----- 318
              ::::||:|::|   |        |:| | |  || : |||              ||
Db        274 ASSYASWIQSKVTELQPRVV----PQTQE-SQPDSNL-CGSHLAFSSAPAQGLLRPILFL 327

Qy        319 TAGPQAGAPSPW 330
                |   | |||
Db        328 PLGLALGLLSPW 339
```

RESULT 3
PSS8_RAT
ID PSS8_RAT STANDARD; PRT; 342 AA.
AC Q9ES87; Q9ER01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prostasin precursor (EC 3.4.21.-).
GN PRSS8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Adachi M., Kitamura K., Miyoshi T., Tomita K.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Wang C.;
RT "Molecular cloning and expression of rat prostasin.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY
CC SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A
CC DISULFIDE BOND (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
CC ITS C-TERMINUS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC ---

CC ---
DR EMBL; AB017638; BAB20281.1; -.
DR EMBL; AF202076; AAG32641.1; -.
DR HSSP; P00734; 1UVS.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
KW Transmembrane.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 32 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
FT PROPEP 323 342 BY SIMILARITY.
FT TRANSMEM 320 340 POTENTIAL.
FT DOMAIN 45 286 SERINE PROTEASE.
FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 168 244 BY SIMILARITY.
FT DISULFID 201 223 BY SIMILARITY.
FT DISULFID 234 262 BY SIMILARITY.
FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 17 17 I -> V (IN REF. 1).
FT CONFLICT 292 292 A -> V (IN REF. 1).
SQ SEQUENCE 342 AA; 36843 MW; 5ED1AF05D9213B98 CRC64;

Query Match 13.6%; Score 422; DB 1; Length 342;
Best Local Similarity 36.2%; Pred. No. 3.4e-21;
Matches 93; Conservative 41; Mismatches 105; Indels 18; Gaps 6;

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Qy         59 GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE 118
              |:  ||:|||| |:   | |:| ||||:: ||::|||||  :  : |   : | ||: | :
Db         49 GSAKPGQWPWQVSITYNGVHVCGGSLVSNQWVVSAAHCFPREHSKE--EYEVKLGAHQLD 106

Qy        119 GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA 174
                 |       || :   :|      |:||::|: | | :    |:|||     || |
Db        107 SFSNDIVVHTVAQIISHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGL 166

Qy        175 SCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGP 230
               | |||       :   |  |: | : |||| ||:|:||       :  :  ||| |
Db        167 HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY 226

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ--- 287
               | :  ||||||||: |   || |  |||:|:  :|   : | : | |: ::||:
Db        227 VKGGKDACQGDSGGPLSC-PIDGLWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV 285

Qy        288 ARVQGAAFLAQSPETPE 304
               | :|  |     |:| |
Db        286 AELQPRAV----PQTQE 298
```

RESULT 4
BSS4_MOUSE
ID BSS4_MOUSE STANDARD; PRT; 306 AA.
AC Q9ER10;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
GN PRSS22 OR PRSS26 OR BSSP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Okui A., Kominami K., Yamaguchi N.;
RT "Cloning and characterization of a novel serine protease, mBSSP-4.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC ---

CC ---
DR EMBL; AB010778; BAB20262.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.252; -.
DR MGD; MGI:1918085; 4733401N09Rik.

```
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    306       BRAIN-SPECIFIC SERINE PROTEASE 4.
FT   ACT_SITE     90     90       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    141    141       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    242    242       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     75     91       BY SIMILARITY.
FT   DISULFID    175    248       BY SIMILARITY.
FT   DISULFID    208    227       BY SIMILARITY.
FT   DISULFID    238    266       BY SIMILARITY.
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   306 AA;  33262 MW;  FBBF03C0C285E7E8 CRC64;

  Query Match             13.4%;  Score 417;  DB 1;  Length 306;
  Best Local Similarity   33.7%;  Pred. No. 6.5e-21;
  Matches  106;  Conservative   55;  Mismatches  114;  Indels   40;  Gaps   13;

Qy          8 SLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTVPGE-- 65
              :| |  :   ||  :|        :|  |: : :     :|     || ::    | ||
Db          9 ALGGDQFSILILLVLL-------TSTAPISAATI-----RVSPDCGKPQQLNRIVGGEDS 56

Qy         66 ----WPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLS 121
                   |||  |: : |:| |:|||: : ||:|||||| |:   : : :||:||: :
Db         57 MDAQWPWIVSILKNGSHHCAGSLLTNRWVVTAAHCF-KSNMDKPSLFSVLLGAWKLGSPG 115

Qy        122 PGAEEVGVAALQLPRAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
             | :::||:| : ||     : :|  :|:||::| |     :    |:|||  : | |
Db        116 PRSQKVGIAWV-LPHPRYSWKEGTHADIALVRLEHSIQFSERILPICLPDSSVRLPPKTD 174

Qy        176 CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPA-RPGMLCGGP 230
              ||  ||    |       | ||: |:: :|    |  :|     |     |   |||| |
Db        175 CWIAGWGSIQDGVPLPHPQTLQKLKVPIIDSELCKSLY----WRGAGQEAITEGMLCAGY 230

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARV 290
              | :  | ||||||::| : | ||:  ||||:   || :| | : |:  || ||:|  |
Db        231 LEGERDACLGDSGGPLMC-QVDDHWLLTGIISWGEGCA-DDRPGVYTSLLAHRSWVQRIV 288

Qy        291 QGA---AFLAQSPET 302
               ||     :|| | :|
Db        289 QGVQLRGYLADSGDT 303


RESULT 5
PSS8_MOUSE
ID   PSS8_MOUSE     STANDARD;      PRT;   342 AA.
AC   Q9ESD1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).
GN   PRSS8 OR CAP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20235202; PubMed=10770960;
RA   Vuagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N.,
RA   Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E.;
RT   "Activation of the amiloride-sensitive epithelial sodium channel by
RT   the serine protease mCAP1 expressed in a mouse cortical collecting
RT   duct cell line.";
RL   J. Am. Soc. Nephrol. 11:828-834(2000).
CC   -!- FUNCTION: POSSESSES A TRYPSIN-LIKE CLEAVAGE SPECIFICITY (BY
CC       SIMILARITY). ACTIVATES AMILORIDE-SENSITIVE SODIUM CHANNELS.
CC   -!- SUBUNIT: HETERODIMER OF TWO CHAINS, LIGHT AND HEAVY, HELD BY A
CC       DISULFIDE BOND (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF
CC       ITS C-TERMINUS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC       FRAMESHIFT IN POSITION 339.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF188613; AAG17054.1; ALT_FRAME.
DR   HSSP; P00734; 1UVS.
DR   MEROPS; S01.158; -.
DR   MGD; MGI:1923810; Prss8.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
KW   Transmembrane.
FT   SIGNAL        1     29       POTENTIAL.
FT   PROPEP       30     32       ACTIVATION PEPTIDE (BY SIMILARITY).
FT   CHAIN        33     44       PROSTATIN LIGHT CHAIN.
FT   CHAIN        45    322       PROSTATIN HEAVY CHAIN.
FT   PROPEP      323    342       BY SIMILARITY.
FT   TRANSMEM    320    340       POTENTIAL.
FT   DOMAIN       45    286       SERINE PROTEASE.
FT   DISULFID     37    154       INTERCHAIN (BY SIMILARITY).
FT   DISULFID     70     86       BY SIMILARITY.
FT   DISULFID    168    244       BY SIMILARITY.
FT   DISULFID    201    223       BY SIMILARITY.
FT   DISULFID    234    262       BY SIMILARITY.
FT   ACT_SITE     85     85       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    134    134       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    238    238       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   342 AA;  36729 MW;  0620DE88ED187D0F CRC64;

  Query Match             13.3%;  Score 414;  DB 1;  Length 342;
  Best Local Similarity   35.2%;  Pred. No. 1.2e-20;
  Matches   92;  Conservative   41;  Mismatches  102;  Indels   26;  Gaps    6;

Qy         59 GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE 118
              |:  ||:|||| |:    | |:| |||:: ||::|||| :  : |  :: | ||: | :
Db         49 GSAKPGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGAHQLD 106

Qy        119 GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA 174
                 |       || :    :|       |:| ::|: | | :    |:|||     || |
Db        107 SYSNDTVVHTVAQIITHSSYREEGSQGDIAFIRLSSPVTFSRYIRPICLPAANASFPNGL 166

Qy        175 SCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGP 230
              | |||        :   |  |: | : |||| ||:|:||       :  : ||| |
Db        167 HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY 226

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW----- 285
              | :  ||||||||: |   :| |  |||:|:  :|   : | : | |: ::||
Db        227 VKGGKDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV 285

Qy        286 --LQARVQGAAFLAQSPETPE 304
                || ||         |:| |
Db        286 AELQPRV--------VPQTQE 298
```

```
RESULT 6
BSS4_HUMAN
ID   BSS4_HUMAN     STANDARD;      PRT;   317 AA.
AC   Q9GZN4; O43342;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
DE   (SP001LA).
GN   PRSS22 OR PRSS26 OR BSSP4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Mitsui S., Okui A., Kominami K., Yamaguchi N.;
RT   "Cloning and characterization of a human brain-specific serine
RT   protease, hBSSP-4.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Wong G.W., Stevens R.L.;
RT   "Identification of a new member of the chromosome 16 family of serine
RT   proteases.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 47-317 FROM N.A.
RA   Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
RA   Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA   Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,
RA   Ueng S., Tatum O., Campbell C., Fawcett J., Deaven L.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB010779; BAB20263.1; -.
DR   EMBL; AF321182; AAG35070.1; -.
DR   EMBL; BC009726; AAH09726.1; -.
DR   EMBL; AC003965; AAB93671.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.252; -.
DR   Genew; HGNC:14368; PRSS22.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Signal.
FT   SIGNAL       1     32       POTENTIAL.
FT   CHAIN       33    317       BRAIN-SPECIFIC SERINE PROTEASE 4.
FT   ACT_SITE    90     90       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   141    141       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   242    242       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    75     91       BY SIMILARITY.
FT   DISULFID   175    248       BY SIMILARITY.
FT   DISULFID   208    227       BY SIMILARITY.
FT   DISULFID   238    266       BY SIMILARITY.
FT   CARBOHYD    70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    47     47       L -> M (IN REF. 4).
SQ   SEQUENCE   317 AA;  33731 MW;  E2A123BC86E79935 CRC64;

  Query Match             12.9%;  Score 400;  DB 1;  Length 317;
  Best Local Similarity   30.8%;  Pred. No. 9.1e-20;
  Matches   99;  Conservative   57;  Mismatches  123;  Indels   42;  Gaps   11;

Qy         27 CIVCITTYAINVSLMWLSFRKVQEPQ--GKAKRHGNTVPG------EWPWQASVRRQGAH 78
              |:   |:  :  |.   |:  ::  |   || ::    | |      ||||  |::: | |
Db         14 CLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQKNGTH 73

Qy         79 ICSGSLVADTWVLTAAHCFEKAAATELNS---WSVVLGSLQREGLSPGAEEVGVAALQLP 135
               |:|||:   ||:||||||:       ||    :||:||: |       :::|||| :: |
Db         74 HCAGSLLTSRWVITAAHCFK----DNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVE-P 128

Qy        136 RAYNHYSQG--SDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW----DQDT 185
                : :|  :|:||::|      :    |:|||  :   |    || :||    |
Db        129 HPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVP 188

Qy        186 SDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGP 245
              | ||: |:: :|    |: :|    :      |    ||| |    | :  | ||||||
Db        189 LPHPQTLQKLKVPIIDSEVCSHLY---WRGAGQGPITEDMLCAGYLEGERDACLGDSGGP 245

Qy        246 VLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEM 305
              ::| : || |: |||||:   ||: : | :  : :|| ||::  |||     ::
Db        246 LMC-QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQ----- 299

Qy        306 SDEDSCVACGSLRTAGPQAGA 326
                      |:||    :||
Db        300 -------GGGALRAPSQGSGA 313


RESULT 7
TRYG_HUMAN
ID   TRYG_HUMAN     STANDARD;      PRT;   321 AA.
AC   Q9NRR2; Q9C015; Q9NRQ8; Q9UBB2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN   TPSG1 OR TMT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
RX   MEDLINE=20302813; PubMed=10843716;
RA   Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
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RA   Wolters P.J., Verghese G.M.;
RT   "Characterization of human gamma-tryptases, novel members of the
RT   chromosome 16p mast cell tryptase and prostasin gene families.";
RL   J. Immunol. 164:6566-6575(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99452974; PubMed=10521469;
RA   Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA   Friend D.S., Krilis S.A., Stevens R.L.;
RT   "Identification of a new member of the tryptase family of mouse and
RT   human mast cell proteases which possesses a novel COOH-terminal
RT   hydrophobic extension.";
RL   J. Biol. Chem. 274:30784-30793(1999).
RN   [3]
RP   SEQUENCE OF 220-321 FROM N.A.
RA   Mittman S., Agnew W.S.;
RT   "Organization and alternative splicing of CACNA1H.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC   -!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
CC       differ by 5 residues.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF191031; AAF76457.1; -.
DR   EMBL; AF195508; AAF76458.1; -.
DR   EMBL; AF175759; AAF03697.1; -.
DR   EMBL; AF175522; AAF03695.1; -.
DR   EMBL; AF223563; AAG48852.2; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.028; -.
DR   Genew; HGNC:14134; TPSG1.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Transmembrane; Polymorphism.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20     36       TRYPTASE GAMMA LIGHT CHAIN.
FT   CHAIN        38    321       TRYPTASE GAMMA HEAVY CHAIN.
FT   TRANSMEM    284    304       POTENTIAL.
FT   ACT_SITE     78     78       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    125    125       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    222    222       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     26    145       INTERCHAIN (POTENTIAL).
FT   DISULFID     63     79       BY SIMILARITY.
FT   DISULFID    159    228       BY SIMILARITY.
FT   DISULFID    192    210       BY SIMILARITY.
FT   DISULFID    218    246       BY SIMILARITY.
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      60     60       M -> V (IN GAMMA-II).
FT                                /FTId=VAR_012097.
FT   VARIANT     126    126       I -> M (IN GAMMA-II).
FT                                /FTId=VAR_012098.
FT   VARIANT     132    132       S -> T (IN GAMMA-II).
FT                                /FTId=VAR_012099.
FT   VARIANT     204    204       L -> I (IN GAMMA-II).
FT                                /FTId=VAR_012100.
FT   VARIANT     288    288       L -> F (IN GAMMA-II).
FT                                /FTId=VAR_012101.
FT   CONFLICT    160    160       W -> S (IN REF. 1).
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SQ   SEQUENCE   321 AA;  33827 MW;  FFF7B06E3C4A962D CRC64;

  Query Match           12.3%;  Score 382;  DB 1;  Length 321;
  Best Local Similarity   35.5%;  Pred. No. 1.4e-18;
  Matches   94;  Conservative   37;  Mismatches   92;  Indels   42;  Gaps    8;

Qy        313 ACG----------SLRTAGPQAGAP----------------SPWPWEARLMHQGQLACG 345
              |||          ||||  |  | |                |||:| | :    ||
Db          5 ACGLLLLLAVPGVSLRTLQPGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRLRRMHVCG 64

Qy        346 GALVSEEAVLTAAHCFIGRQAPEEWSVGLG-----TRPEEWGLKQLILHGAYT-HPEGGY 399
              |:|:| : |||||||| |     :: | ||       |    ::|:||| : :  |
Db         65 GSLLSPQWVLTAAHCFSGSLNSSDYQVHLGELEITLSPHFSTVRQIILHSSPSGQPGTSG 124

Qy        400 DMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERGWVL--GRARPGAGIS---SLQTVPV 454
              |:||: |: |||| : : |:|||         | | ||   |  | |  :    ||: | |
Db        125 DIALVELSVPVTLSSRILPVCLPEASDDFCPGIRCWVTGWGYTREGEPLPPPYSLREVKV 184

Qy        455 TLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLH 514
              :::    | | :  ||  || : | |:|    |: :|:  || ||| :| | |  ||:.
Db        185 SVVDTETCRRDYPGPG--GSILQPDMLCARGPGD--ACQDDSGGPLVCQVNGAWVQAGIV 240

Qy        515 SFGDACQGPARPAVFTALPAYEDWV 539
              |:|: |  | || |:| :||| :|:
Db        241 SWGEGCGRPNRPGVYTRVPAYVNWI 265


RESULT 8
PLMN_MOUSE
ID   PLMN_MOUSE     STANDARD;      PRT;   812 AA.
AC   P20918; Q8CIS2; Q91WJ5;
DT   01-FEB-1991 (Rel. 17, Created)
DT   15-SEP-2003 (Rel. 42, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN   PLG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91184812; PubMed=2081600;
RA   Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
RT   "Characterization of the cDNA coding for mouse plasminogen and
RT   localization of the gene to mouse chromosome 17.";
RL   Genomics 8:49-61(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA   Nagaraja R.;
RT   "Genomic sequence analysis in the mouse t-complex region.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 1-16 FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Liver;
RX   PubMed=12149246;
RA   Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA   Parmer R.J., Miles L.A.;
RT   "Localization of regulatory elements mediating constitutive and
RT   cytokine-stimulated plasminogen gene expression.";
RL   J. Biol. Chem. 277:38579-38588(2002).
RN   [5]
RP   CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX   MEDLINE=95042728; PubMed=7525077;
RA   O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA   Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT   "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT   suppression of metastases by a Lewis lung carcinoma.";
RL   Cell 79:315-328(1994).
CC   -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC       A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC       EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC       AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC       GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC       ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC       AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC       LAMININ AND VON WILLEBRAND FACTOR.
CC   -!- FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS
CC       NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
CC       METASTATIC TUMORS IN VIVO.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC       higher selectivity than trypsin. Converts fibrin into soluble
CC       products.
CC   -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC       ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC       FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC   -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC       IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC   -!- MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION
CC       INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD
CC       TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE
CC       ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC   -!- SIMILARITY: Contains 5 kringle domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04766; AAA50168.1; -.
DR   EMBL; AF481053; AAM22156.1; -.
DR   EMBL; BC014773; AAH14773.1; -.
DR   EMBL; AY134430; AAN15805.1; -.
DR   PIR; A38514; PLMS.
DR   HSSP; P00747; 1PMK.
DR   MEROPS; S01.233; -.
DR   MGD; MGI:97620; Plg.
DR   GO; GO:0016506; F:apoptosis activator activity; IDA.
DR   GO; GO:0006915; P:apoptosis; IDA.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR003966; Prothrombin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00051; kringle; 5.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 5.
DR   SMART; SM00130; KR; 5.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 5.
DR   PROSITE; PS50070; KRINGLE_2; 5.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW   Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW   Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    812       PLASMINOGEN.
FT   CHAIN        20    581       PLASMIN HEAVY CHAIN A.
FT   PEPTIDE      20     97       ACTIVATION PEPTIDE.
FT   CHAIN        98    581       PLASMIN SHORT FORM OF CHAIN A.
FT   CHAIN        98   ?436       ANGIOSTATIN.
FT   CHAIN       582    812       PLASMIN LIGHT CHAIN B.
FT   DOMAIN      103    181       KRINGLE 1.
FT   DOMAIN      184    262       KRINGLE 2.
FT   DOMAIN      275    352       KRINGLE 3.
FT   DOMAIN      377    454       KRINGLE 4.
FT   DOMAIN      481    560       KRINGLE 5.
FT   DOMAIN      582    812       SERINE PROTEASE.
FT   ACT_SITE    624    624       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    667    667       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    762    762       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID     49     73       BY SIMILARITY.
FT   DISULFID     53     61       BY SIMILARITY.
FT   DISULFID    103    181       BY SIMILARITY.
FT   DISULFID    124    164       BY SIMILARITY.
FT   DISULFID    152    176       BY SIMILARITY.
FT   DISULFID    185    262       BY SIMILARITY.
FT   DISULFID    188    316       BY SIMILARITY.
FT   DISULFID    206    245       BY SIMILARITY.
FT   DISULFID    234    257       BY SIMILARITY.
FT   DISULFID    275    352       BY SIMILARITY.
FT   DISULFID    296    335       BY SIMILARITY.
FT   DISULFID    324    347       BY SIMILARITY.
FT   DISULFID    377    454       BY SIMILARITY.
FT   DISULFID    398    437       BY SIMILARITY.
FT   DISULFID    426    449       BY SIMILARITY.
FT   DISULFID    481    560       BY SIMILARITY.
FT   DISULFID    502    543       BY SIMILARITY.
FT   DISULFID    531    555       BY SIMILARITY.
FT   DISULFID    568    687       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    578    586       INTERCHAIN (BY SIMILARITY).
FT   DISULFID    609    625       BY SIMILARITY.
FT   DISULFID    701    768       BY SIMILARITY.
FT   DISULFID    731    747       BY SIMILARITY.
FT   DISULFID    758    786       BY SIMILARITY.
FT   CONFLICT    235    235       R -> H (IN REF. 1).
FT   CONFLICT    525    525       G -> D (IN REF. 1).
FT   CONFLICT    649    649       S -> L (IN REF. 1).
SQ   SEQUENCE   812 AA;  90781 MW;  24173260E6A2FFD2 CRC64;

  Query Match          12.0%;  Score 371.5;  DB 1;  Length 812;
  Best Local Similarity  32.7%;  Pred. No. 2e-17;
  Matches   93;  Conservative   45;  Mismatches  107;  Indels   39;  Gaps   11;

Qy        23 LYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVRRQ 75
             |||:| : :   |        |  :  :|| : |:  |  |       |  |||| |:| :
Db       551 LYDYCDIPLCASA--------SSFECGKPQVEPKKCPGRVVGGCVANPHSWPWQISLRTR 602

Qy        76 --GAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
               | | | |:|:|  ||||||| ||::  |   : |:||: :        :|: || |
Db       603 FTGQHFCGGTLIAPEWVLTAAHCLEKSSRPEF--YKVILGAHEEYIRGSDVQEISVAKLI 660
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Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTSD 187
Db        661 LE------PNNRDIALLKLSRPATITDKVIPACLPSPNYMVADRTICYITGWGETQGTFG 714

Qy        188 APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 247
Db        715 A-GRLKEAQLPVIENKVCNRV------EYLNNRVKSTELCAGQLAGGVDSCQGDSGGPLV 767

Qy        248 CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQ 291
Db        768 CFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVDWIEREMR 810


RESULT 9
PLMN_PIG
ID   PLMN_PIG      STANDARD;      PRT;   790 AA.
AC   P06867;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Plasminogen (EC 3.4.21.7).
GN   PLG.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE OF 1-560.
RA   Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.E.;
RT   "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
RT   of the carbohydrate attachment sites with the human and bovine
RT   species.";
RL   Fibrinolysis 1:91-102(1987).
RN   [2]
RP   SEQUENCE OF 450-790.
RX   MEDLINE=85203907; PubMed=3846533;
RA   Marti T., Schaller J., Rickli E.E.;
RT   "Determination of the complete amino-acid sequence of porcine
RT   miniplasminogen.";
RL   Eur. J. Biochem. 149:279-285(1985).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=88185329; PubMed=3356193;
RA   Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA   Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
RT   "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT   plasminogen. Species specificity in relation to sialylation and
RT   fucosylation patterns.";
RL   Eur. J. Biochem. 173:57-63(1988).
CC   -!- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
CC       A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
CC       EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
CC       AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
CC       GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
CC       ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
CC       AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
CC       LAMININ AND VON WILLEBRAND FACTOR.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC       higher selectivity than trypsin. Converts fibrin into soluble
CC       products.
CC   -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
CC       ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
CC       FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
CC   -!- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SIALIC ACID AND
CC       IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC
CC       DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
CC       (MICROHETEROGENEITY).
CC   -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
CC       IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.
CC   -!- SIMILARITY: Contains 5 kringle domains.
DR   PIR; S03733; PLPG.
DR   HSSP; P00747; 5HPG.
DR   MEROPS; S01.233; -.
DR   GlycoSuiteDB; P06867; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR003014; PAN.
DR   InterPro; IPR003609; Pan_app.
DR   InterPro; IPR003966; Prothrombin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00051; kringle; 5.
DR   Pfam; PF00024; PAN; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR01505; PROTHROMBIN.
DR   ProDom; PD000395; Kringle; 5.
DR   SMART; SM00130; KR; 5.
DR   SMART; SM00473; PAN_AP; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS00021; KRINGLE_1; 5.
DR   PROSITE; PS50070; KRINGLE_2; 5.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW   Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT   CHAIN         1    560       PLASMIN HEAVY CHAIN A.
FT   CHAIN       561    790       PLASMIN LIGHT CHAIN B.
FT   DOMAIN      561    790       SERINE PROTEASE.
FT   DOMAIN       84    162       KRINGLE 1.
FT   DOMAIN      166    243       KRINGLE 2.
FT   DOMAIN      256    333       KRINGLE 3.
FT   DOMAIN      358    435       KRINGLE 4.
FT   DOMAIN      461    540       KRINGLE 5.
FT   ACT_SITE    602    602       CHARGE RELAY SYSTEM.
FT   ACT_SITE    645    645       CHARGE RELAY SYSTEM.
FT   ACT_SITE    740    740       CHARGE RELAY SYSTEM.
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000019.
FT   CARBOHYD    340    340       O-LINKED (GALNAC. . .).
FT                                /FTId=CAR_000020.
SQ   SEQUENCE   790 AA;  88592 MW;  F04EA06E74BCD58E CRC64;

  Query Match             11.9%;  Score 370.5;  DB 1;  Length 790;
  Best Local Similarity   32.3%;  Pred. No. 2.2e-17;
  Matches   90;  Conservative   49;  Mismatches  101;  Indels   39;  Gaps   12;

Qy         23 LYDFCIV--CITTYAINVSLMWLSF----RKVQEPQGKAKRHGN--TVPGEWPWQASVR- 73
Db        531 LFDYCDVPQCVTS----------SFDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRY 580

Qy         74 RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQ 133
Db        581 RYRGHFCGGTLISPEWVLTAKHCLEKSSSP--SSYKVILGAHEEYHLGEGVQEIDVSKL- 637

Qy        134 LPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGWDQDTSD-A 188
Db        638 ----FKEPSE-ADIALLKLSSPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYG 692

Qy        189 PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC 248
Db        693 AGLLKEARLPVIENKVCN------RYEYLGGKVSPNELCAGHLAGGIDSCQGDSGGPLVC 746

Qy        249 LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
Db        747 FEKDKYILQ-GVTSWGLGCALPNKPGVYVRVSRFVTWIE 784


RESULT 10
TEST_MOUSE
ID   TEST_MOUSE     STANDARD;      PRT;   324 AA.
AC   Q9JHJ7; Q9DA14;
DT   16-OCT-2001 (Rel. 40, Created)
```

```
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Testisin precursor (EC 3.4.21.-) (Tryptase 4).
GN   PRSS21.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=21153229; PubMed=11231276;
RA   Scarman A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C.,
RA   Normyle J.F., Antalis T.M.;
RT   "Organization and chromosomal localization of the murine Testisin gene
RT   encoding a serine protease temporally expressed during
RT   spermatogenesis.";
RL   Eur. J. Biochem. 268:1250-1258(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Testis;
RX   PubMed=11259427;
RA   Wong G.W., Li L., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
RA   Rothenberg M.E., Sali A., Stevens R.L.;
RT   "Tryptase 4, a new member of the chromosome 17 family of mouse serine
RT   proteases.";
RL   J. Biol. Chem. 276:20648-20658(2001).
RN   [3]
RP   SEQUENCE OF 3-324 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: COULD REGULATE PROTEOLYTIC EVENTS ASSOCIATED WITH
CC       TESTICULAR GERM CELL MATURATION.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- TISSUE SPECIFICITY: Testis.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN POST-MEIOTIC TESTICULAR GERM
CC       CELLS.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP
CC       CODON IN POSITION 315.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF304012; AAK29360.1; -.
DR   EMBL; AY005145; AAG02255.1; -.
DR   EMBL; AF176209; AAF64407.2; -.
DR   EMBL; AF226710; AAF64428.2; -.
DR   EMBL; AK006271; -; NOT_ANNOTATED_CDS.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.011; -.
DR   MGD; MGI:1916698; Prss21.
DR   GO; GO:0005624; C:membrane fraction; IDA.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen.
FT   SIGNAL       1     21       POTENTIAL.
FT   PROPEP      22     54       POTENTIAL.
FT   CHAIN       55    298       TESTISIN.
FT   PROPEP     299    324       REMOVED IN MATURE FORM (POTENTIAL).
FT   ACT_SITE    95     95       CHARGE RELAY SYSTEM (POTENTIAL).
FT   ACT_SITE   147    147       CHARGE RELAY SYSTEM (POTENTIAL).
FT   ACT_SITE   248    248       CHARGE RELAY SYSTEM (POTENTIAL).
FT   DISULFID    46    167       POTENTIAL.
FT   DISULFID    80     96       POTENTIAL.
FT   DISULFID   181    254       POTENTIAL.
FT   DISULFID   214    233       POTENTIAL.
FT   DISULFID   244    272       POTENTIAL.
FT   LIPID      298    298       GPI-ANCHOR (POTENTIAL).
FT   CARBOHYD   170    170       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   283    283       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   275    275       P -> H (IN REF. 3).
SQ   SEQUENCE   324 AA;  36175 MW;  56DC59E84F3C3CD4 CRC64;

  Query Match           11.9%;  Score 368.5;  DB 1;  Length 324;
  Best Local Similarity  29.2%;  Pred. No. 1.1e-17;
  Matches   88;  Conservative   56;  Mismatches  122;  Indels   35;  Gaps   10;

Qy         28 IVCITTYAINVSLMWLSF----RKVQEPQGKAKRHGN-TVP----------GEWPWQAS 71
              :| : | |: :   :|       ::|||   :   |: |:|          | |||| |
Db         12 LVVVATAAMALQSTYLQVDPEKPELQEPDLLSGPCGHRTIPSRIVGGDDAELGRWPWQGS 71

Qy         72 VRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE----GLSPGAEEV 127
              :|  | |:|  :|:   |||||||||:|    :   |:|  | |       |   :
Db         72 LRVWGNHLCGATLLNRRWVLTAAHCFQK--DNDPFDWTVQFGELTSRPSLWNLQAYSNRY 129

Qy        128 GVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW-- 181
              :  : |   |:     :|:|||:|: | |:     |:||    ::|     || |||
Db        130 QIEDIFLSPKYSE-QYPNDIALLKLSSPVTYNNFIQPICLLNSTYKFENRTDCWVTGWGA 188

Qy        182 --DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQ 239
                : ::  :| ||: ::: :|:   || :| :   |         |:| |   | :  |
Db        189 IGEDESLPSPNTLQEVQVAIINNSMCNHMYKKPDFR---TNIWGDMVCAGTPEGGKDACF 245

Qy        240 GDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQS 299
              ||||||: | : |  | | |::|:   | : : | : || : | :|:|: :      |
Db        246 GDSGGPLAC-DQDTVWYQVGVVSWGIGCGRPNRPGVYTNISHHYNWIQSTMIRNGLLRPD 304

Qy        300 P 300
              |
Db        305 P 305


RESULT 11
ST14_MOUSE
ID   ST14_MOUSE     STANDARD;      PRT;   855 AA.
AC   P56677;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Epithin).
GN   ST14 OR PRSS14.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C.B.17SCID; TISSUE=Thymus;
RX   MEDLINE=99216440; PubMed=10199918;
RA   Kim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C.,
RA   Schwartz R.H.;
RT   "Cloning and chromosomal mapping of a gene isolated from thymic
RT   stromal cells encoding a new mouse type II membrane serine protease,
RT   epithin, containing four LDL receptor modules and two CUB domains.";
RL   Immunogenetics 49:420-428(1999).
RN   [2]
RP   REVISIONS TO 23; 321; 325; 343; 409-410 AND C-TERMINUS.
RC   STRAIN=C.B.17SCID; TISSUE=Thymus;
RA   Kim M.G., Chen C., Cho E.G., Park D., Schwartz R.H.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN INTESTINE, KIDNEY, LUNG,
CC       AND THYMUS. NOT EXPRESSED IN SKELETAL MUSCLE, LIVER, HEART,
CC       TESTIS, AND BRAIN.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 2 CUB domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF042822; AAD02230.3; -.
DR   EMBL; BC005496; AAH05496.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.302; -.
DR   MGD; MGI:1338881; St14.
DR   GO; GO:0005576; C:extracellular; IDA.
DR   GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000859; CUB_domain.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 4.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00192; LDLa; 4.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS01209; LDLRA_1; 2.
DR   PROSITE; PS50068; LDLRA_2; 4.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
KW   Transmembrane; Repeat.
FT   DOMAIN        1     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     76       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       77    855       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      214    331       CUB 1.
FT   DOMAIN      340    444       CUB 2.
FT   DOMAIN      451    488       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN      489    522       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN      523    561       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN      565    604       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN      615    854       SERINE PROTEASE.
FT   ACT_SITE    656    656       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    711    711       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    805    805       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    302    302       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    365    365       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    421    421       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    772    772       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   855 AA;  94654 MW;  4F10E84DA2146DD5 CRC64;

  Query Match             11.9%;  Score 368.5;  DB 1;  Length 855;
  Best Local Similarity   32.8%;  Pred. No. 3.3e-17;
  Matches   85;  Conservative   38;  Mismatches  105;  Indels   31;  Gaps    8;

Qy         44 SFRKVQEPQGKAKRHGNTVPGEWPWQASVRRQG-AHICSGSLVADTWVLTAAHCFE---K 99
              || |    | :    |   ||||||:|:   |  |:|  ||::  |:::|||||:
Db        608 SFTK----QARVVGGTNADEGEWPWQVSLHALGQGHLCGASLISPDWLVSAAHCFQDDKN 663

Qy        100 AAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPR-----AYNHYSQGSDLALLQL-- 152
                 ::   |:  || | :   |       ||   |:| |     ::| ::   |:|||:|
Db        664 FKYSDYTMWTAFLGLLDQSKRSAS----GVQELKLKRIITHPSFNDFTFDYDIALLELEK 719

Qy        153 --AHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSDAPGT--LRNLRLRLISRPTCNCI 208
               : |   |:|||   | || | : | |||         |   |:   :|:|:: ||  :
Db        720 SVEYSTVVRPICLPDATHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEDL 779

Qy        209 YNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCA 268
               |           | |:| |   |    ||||||||:   | ||   |||::|:   ||
Db        780 MPQ--------QITPRMMCVGFLSGGVDSCQGDSGGPLSSAEKDGRMFQAGVVSWGEGCA 831

Qy        269 QEDAPVLLTNTAAHSSWLQ 287
              | : | : |       |::
Db        832 QRNKPGVYTRLPVVRDWIK 850


RESULT 12
TRYG_MOUSE
ID   TRYG_MOUSE     STANDARD;      PRT;   311 AA.
AC   Q9QUL7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN   TPSG1 OR TMT.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv, and BALB/c;
RX   MEDLINE=99452974; PubMed=10521469;
RA   Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA   Friend D.S., Krilis S.A., Stevens R.L.;
RT   "Identification of a new member of the tryptase family of mouse and
RT   human mast cell proteases which possesses a novel COOH-terminal
RT   hydrophobic extension.";
RL   J. Biol. Chem. 274:30784-30793(1999).
CC   -!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF175760; AAF03698.1; -.
DR   EMBL; AF175523; AAF03696.1; -.
DR   HSSP; P20231; 1AAO.
DR   MEROPS; S01.028; -.
DR   MGD; MGI:1349391; Tpsg1.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; FALSE_NEG.
KW   Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW   Transmembrane.
FT   SIGNAL       1     16       POTENTIAL.
FT   CHAIN       17     28       TRYPTASE GAMMA LIGHT CHAIN.
FT   CHAIN       30    311       TRYPTASE GAMMA HEAVY CHAIN.
FT   TRANSMEM   277    297       POTENTIAL.
FT   ACT_SITE    70     70       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   117    117       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE   214    214       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   DISULFID    18    137       INTERCHAIN (POTENTIAL).
FT   DISULFID    55     71       BY SIMILARITY.
FT   DISULFID   151    220       BY SIMILARITY.
FT   DISULFID   184    202       BY SIMILARITY.
FT   DISULFID   210    238       BY SIMILARITY.
FT   CARBOHYD    77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   192    192       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   311 AA;  32656 MW;  7FC9D6EF6A2A8808 CRC64;

  Query Match           11.7%;  Score 363;  DB 1;  Length 311;
  Best Local Similarity  34.7%;  Pred. No. 2.5e-17;
  Matches   86;  Conservative   42;  Mismatches   98;  Indels   22;  Gaps    6;

Qy        303 PEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFI 362
              |::|:  |       |  |  |     |||:| |       |||:|:| | ||||||||
Db         21 PQVSNSGS-------RIVGGHAAPAGTWPWQASLRLHKVHVCGGSLLSPEWVLTAAHCFS 73

Qy        363 GRQAPEEWSVGLG-----TRPEEWGLKQLILHGAYTHPEGGY-DMALLLLAQPVTLGASL 416
              |     :: | ||       |    :|::|::     | |   |:||: |: || | : :
Db         74 GSVNSSDYQVHLGELTVTLSPHFSTVKRIIMYTGSPGPPGSSGDIALVQLSSPVALSSQV 133

Qy        417 RPLCLPYPDHHLPDGERGWVLGRARPGAGIS-----SLQTVPVTLLGPRACSRLHAAPGG 471
              :|:|||        | : || |    | |       :||    |:::  : ||: : :|
Db        134 QPVCLPEASADFYPGMQCWVTGWGYTGEGEPLKPPYNLQEAKVSVVDVKTCSQAYNSP-- 191

Qy        472 DGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTA 531
              :|| | | |:|    |:  :|:  || ||| :| |||  ||: |:|: |  | || |:
Db        192 NGSLIQPDMLCARGPGD--ACQDDSGGPLVCQVAGTWQQAGVVSWGEGCGRPDRPGVYAR 249

Qy        532 LPAYEDWV 539

              : || :|:
Db        250 VTAYVNWI 257


RESULT 13
ST14_HUMAN
ID   ST14_HUMAN     STANDARD;      PRT;   855 AA.
AC   Q9Y5Y6; Q9BS01; Q9H3S0; Q9HB36; Q9HCA3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-
DE   type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15)
DE   (Tumor associated differentially-expressed gene-15 protein).
GN   ST14 OR PRSS14 OR SNC19 OR TADG15.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99303581; PubMed=10373424;
RA   Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
RT   "Molecular cloning of cDNA for matriptase, a matrix-degrading serine
RT   protease with trypsin-like activity.";
RL   J. Biol. Chem. 274:18231-18236(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99432178; PubMed=10500122;
RA   Takeuchi T., Shuman M.A., Craik C.S.;
RT   "Reverse biochemistry: Use of macromolecular protease inhibitors to
RT   dissect complex biological processes and identify a membrane-type
RT   serine protease in epithelial cancer and normal tissue.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Prostate;
RA   Yamaguchi N., Mitsui S.;
RT   "Molecular cloning of a novel transmembrane serine protease expressed
RT   in human prostate.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Tanimoto H., Underwood L.J., Wang Y., Shigemasa K., Parmley T.H.,
RA   O'Brien T.J.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 327-855 FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 340-664 FROM N.A.
RA   Cao J., Fan W., Zheng S.;
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RT   "Genomic analysis of a novel human serine protease SNC19.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   CHARACTERIZATION.
RC   TISSUE=Milk;
RX   MEDLINE=99303582; PubMed=10373425;
RA   Lin C.Y., Anders J., Johnson M., Dickson R.B.;
RT   "Purification and characterization of a complex containing matriptase
RT   and a Kunitz-type serine protease inhibitor from human milk.";
RL   J. Biol. Chem. 274:18237-18242(1999).
CC   -!- FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE
CC       IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE
CC       ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUBSTRATES WITH ARG
CC       OR LYS AS THE P1 SITE.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 2 CUB domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF118224; AAD42765.2; -.
DR   EMBL; AF133086; AAF00109.1; -.
DR   EMBL; AB030036; BAB20376.1; -.
DR   EMBL; AF057145; AAG15395.1; -.
DR   EMBL; BC005826; AAH05826.1; -.
DR   EMBL; AF283256; AAG13949.1; -.
DR   HSSP; P00763; 1DPO.
DR   Genew; HGNC:11344; ST14.
DR   MIM; 606797; -.
DR   MEROPS; S01.302; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000859; CUB_domain.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00057; ldl_recept_a; 4.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00192; LDLa; 3.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS01209; LDLRA_1; 2.
DR   PROSITE; PS50068; LDLRA_2; 4.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
KW   Transmembrane; Repeat.
FT   DOMAIN        1     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     76       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       77    855       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN      214    334       CUB 1.
FT   DOMAIN      340    447       CUB 2.
FT   DOMAIN      452    487       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN      487    524       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN      524    560       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN      566    603       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN      615    854       SERINE PROTEASE.
FT   ACT_SITE    656    656       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    711    711       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    805    805       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    302    302       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    485    485       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    772    772       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    327    329       FEA -> GTR (IN REF. 5).
FT   CONFLICT    381    381       R -> S (IN REF. 4).
FT   CONFLICT    674    674       A -> V (IN REF. 3).
SQ   SEQUENCE   855 AA;  94769 MW;  26143132C01F99C9 CRC64;

  Query Match             11.6%;  Score 361.5;  DB 1;  Length 855;
  Best Local Similarity   33.6%;  Pred. No. 9.6e-17;
  Matches   79;  Conservative   41;  Mismatches   96;  Indels   19;  Gaps    7;

Qy         64 GEWPWQASVRRQG-AHICSGSLVADTWVLTAAHCF---EKAAATELNSWSVVLG-SLQRE 118
              |||||| |:   |  |||  ||::  |:::||||:        ::   |:  ||   | :
Db        624 GEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQ 683

Qy        119 GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA 174
                :|| :|  :  :     :| ::   |:|||:|  |  ::    |:|||  :| || |
Db        684 RSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGK 743

Qy        175 SCWATGWDQDTSDAPGT--LRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQP 232
              : | |||        |   |:  :|:|:: ||    | | |:       | |:| |
Db        744 AIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE---NLLPQQ-----ITPRMMCVGFLS 795

Qy        233 GVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              |    ||||||||:  :| ||   |||::|:   ||| : | : |       |::
Db        796 GGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIK 850


RESULT 14
PLMN_HUMAN
ID   PLMN_HUMAN     STANDARD;      PRT;   810 AA.
AC   P00747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN   PLG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90202879; PubMed=2318848;
RA   Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
RT   "Characterization of the gene for human plasminogen, a key proenzyme
RT   in the fibrinolytic system.";
RL   J. Biol. Chem. 265:6104-6111(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87162490; PubMed=3030813;
RA   Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;
RT   "Molecular cloning and characterization of a full-length cDNA clone
RT   for human plasminogen.";
RL   FEBS Lett. 213:254-260(1987).
RN   [3]
RP   SEQUENCE OF 20-810.
RA   Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL   Submitted (JUL-1977) to the PIR data bank.
RN   [4]
RP   SEQUENCE OF 292-810 FROM N.A.
RX   MEDLINE=85023311; PubMed=6148961;
RA   Malinowski D.P., Sadler J.E., Davie E.W.;
RT   "Characterization of a complementary deoxyribonucleic acid coding for
RT   human and bovine plasminogen.";
RL   Biochemistry 23:4243-4250(1984).
RN   [5]
RP   SEQUENCE OF 20-100.
RX   MEDLINE=75093329; PubMed=122932;
RA   Wiman B., Wallen P.;
RT   "Structural relationship between 'glutamic acid' and 'lysine' forms
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RT of human plasminogen and their interaction with the NH2-terminal
RT activation peptide as studied by affinity chromatography.";
RL Eur. J. Biochem. 50:489-494(1975).
RN [6]
RP SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810.
RA Sottrup-Jensen L., Claeys H., Zajdel M., Petersen T.E., Magnusson S.;
RL (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
RL Raven Press, New York (1978).
RN [7]
RP SEQUENCE OF 483-604.
RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN [8]
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN [9]
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4694729;
RA Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN [10]
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Groskopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [11]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Trexler M., Vali Z., Patthy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Vali Z., Patthy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;
RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [14]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevich R., Nacy C.A.;
RT "A recombinant human angiostatin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid.";
RL Biochemistry 35:2567-2576(1996).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [23]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; PubMed=8181475;
RA Rejante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; PubMed=8181476;
RA Rejante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [25]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; PubMed=8652577;
RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;

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RT   "Recombinant gene expression and 1H NMR characteristics of the
RT   kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT   of plasminogen kringle domains.";
RL   Biochemistry 35:2357-2364(1996).
RN   [26]
RP   STRUCTURE BY NMR OF 374-461.
RX   MEDLINE=90219023; PubMed=2157850;
RA   Atkinson R.A., Williams R.J.P.;
RT   "Solution structure of the kringle 4 domain from human plasminogen by
RT   1H nuclear magnetic resonance spectroscopy and distance geometry.";
RL   J. Mol. Biol. 212:541-552(1990).
RN   [27]
RP   VARIANTS PHE-374 AND THR-620.

  Query Match            11.6%;  Score 359.5;  DB 1;  Length 810;
  Best Local Similarity   33.8%;  Pred. No. 1.2e-16;
  Matches   95;  Conservative   39;  Mismatches  104;  Indels   43;  Gaps   13;

Qy         23 LYDFCIV--CITTYAINVSLMWLSFRKVQEPQGKAKR-HGNTV------PGEWPWQASVR 73
              |||:| |  |              ||    :|| : |:  |  |      |  |||| |:|
Db        551 LYDYCDVPQCAAP----------SF-DCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLR 599

Qy         74 -RQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAAL 132
               | | | | |:|::  |||||||| ||:     :|: |:||: |   |  |  :|: |: |
Db        600 TRFGMHFCGGTLISPEWVLTAAHCLEKSPRP--SSYKVILGAHQEVNLEPHVQEIEVSRL 657

Qy        133 QLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWATGW--DQDTS 186
               |           |:|||:|: |   |    | ||| | :       |: |||   | |
Db        658 FLE------PTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTF 711

Qy        187 DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPV 246
               | | |:  :| :|    ||          |:   :   || |   |    ||||||||:
Db        712 GA-GLLKEAQLPVIENKVCN------RYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPL 764

Qy        247 LCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQ 287
              :| | | : :| |: |:   ||: : :| :    :   :|::
Db        765 VCFEKDKYILQ-GVTSWGLGCARPNKPGVYVRVSRFVTWIE 804


RESULT 15
TMS3_HUMAN
ID   TMS3_HUMAN     STANDARD;      PRT;   454 AA.
AC   P57727;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Transmembrane protease, serine 3 (EC 3.4.21.-) (Serine protease
DE   TADG-12) (Tumor associated differentially-expressed gene-12 protein).
GN   TMPRSS3 OR TADG12 OR ECHOS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS A AND T).
RC   TISSUE=Ovarian carcinoma;
RX   MEDLINE=20521358; PubMed=11068177;
RA   Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,
RA   Wang Y., Parmley T.H., O'Brien T.J.;
RT   "Ovarian tumor cells express a novel multi-domain cell surface serine
RT   protease.";
RL   Biochim. Biophys. Acta 1502:337-350(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS A; B AND D), AND VARIANT ILE-53.
RX   MEDLINE=20578749; PubMed=11137999;
RA   Scott H.S., Kudoh J., Wattenhofer M., Shibuya K., Berry A., Chrast R.,
RA   Guipponi M., Wang J., Kawasaki K., Asakawa S., Minoshima S.,
RA   Younus F., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C.,
RA   Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B.,
RA   Antonarakis S.E.;
RT   "Insertion of beta-satellite repeats identifies a transmembrane
RT   protease causing both congenital and childhood onset autosomal
RT   recessive deafness.";
RL   Nat. Genet. 27:59-63(2001).
RN   [3]
RP   SUBCELLULAR LOCATION, AND FUNCTION IN ENAC CLEAVAGE.
RX   PubMed=12393794;
RA   Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M.,
RA   Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M.,
RA   Buchet K., Reymond A., Hummler E., Marzella P.L., Kudoh J.,
RA   Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.;
RT   "The transmembrane serine protease (TMPRSS3) mutated in deafness
RT   DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro.";
RL   Hum. Mol. Genet. 11:2829-2836(2002).
RN   [4]
RP   VARIANTS DFBN8/DFNB10 CYS-251 AND LEU-404.
RX   MEDLINE=21354482; PubMed=11462234;
RA   Masmoudi S., Antonarakis S.E., Schwede T., Ghorbel A.M., Gratri M.,
RA   Pappasavas M.P., Drira M., Elgaied-Boulila A., Wattenhofer M.,
RA   Rossier C., Scott H.S., Ayadi H., Guipponi M.;
RT   "Novel missense mutations of TMPRSS3 in two consanguineous Tunisian
RT   families with non-syndromic autosomal recessive deafness.";
RL   Hum. Mutat. 18:101-108(2001).
RN   [5]
RP   VARIANTS DFBN8/DFNB10 TRP-109; PHE-194 AND ARG-407, AND VARIANTS
RP   ILE-53; SER-111 AND VAL-253.
RX   MEDLINE=21317610; PubMed=11424922;
RA   Ben-Yosef T., Wattenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S.,
RA   Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B.,
RA   Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A.,
RA   Nance W.E., Wilcox E.R., Friedman T.B., Morell R.J.;
RT   "Novel mutations of TMPRSS3 in four DFNB8/B10 families segregating
RT   congenital autosomal recessive deafness.";
RL   J. Med. Genet. 38:396-400(2001).
RN   [6]
RP   VARIANT DFBN8/DFNB10 GLY-103, AND VARIANTS ASN-173 AND THR-426.
RX   MEDLINE=21904597; PubMed=11907649;
RA   Wattenhofer M., Di Iorio V., Rabionet R., Dougherty L., Pampanos A.,
RA   Schwede T., Montserrat-Sentis B., Arbones L., Iliades T.,
RA   Pasquadibisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M.,
RA   Petersen M.B., Estivill X., Gasparini P., Scott H.S.,
RA   Antonarakis S.E.;
RT   "Mutations in the TMPRSS3 gene are a rare cause of childhood
RT   nonsyndromic deafness in Caucasian patients.";
RL   J. Mol. Med. 80:124-131(2002).
CC   -!- FUNCTION: Probable protease. Seems to be capable of activating
CC       ENaC.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC       reticulum.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P57727-1; Sequence=Displayed;
CC       Name=B; Synonyms=C;
CC         IsoId=P57727-2; Sequence=VSP_005391;
CC       Name=D;
CC         IsoId=P57727-3; Sequence=VSP_005392;
CC       Name=T; Synonyms=Truncated, TADG-12V;
CC         IsoId=P57727-4; Sequence=VSP_005393, VSP_005394;
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues including fetal
CC       cochlea. Isoform T is found at increased levels in some
CC       carcinomas.
CC   -!- PTM: Undegoes autoproteolytic activation.
CC   -!- DISEASE: Defects in TMPRSS3 are a cause of childhood-onset
CC       autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072].
CC   -!- DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal
CC       recessive neurosensory deafness 10 (DFNB10) [MIM:605316].
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: Contains 1 SRCR domain.
CC   -!- SIMILARITY: Contains 1 LDL-receptor class A domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AF201380; AAG37012.1; -.
DR   EMBL; AB038157; BAB20077.1; -.
DR   EMBL; AB038158; BAB20078.1; -.
DR   EMBL; AB038159; BAB20079.1; -.
DR   EMBL; AB038160; BAB20080.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.079; -.
DR   Genew; HGNC:11877; TMPRSS3.
DR   MIM; 605511; -.
DR   MIM; 601072; -.
DR   MIM; 605316; -.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   InterPro; IPR001190; Srcr_receptor.
DR   Pfam; PF00057; ldl_recept_a; 1.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00192; LDLa; 1.
DR   SMART; SM00202; SR; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 1.
DR   PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR   PROSITE; PS50287; SRCR_2; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen;
KW   Endoplasmic reticulum; Deafness; Alternative splicing;
KW   Disease mutation; Polymorphism.
FT   DOMAIN        1     48       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     49     69       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT                                (POTENTIAL).
FT   DOMAIN       70    454       EXTRACELLULAR (POTENTIAL).
FT   DOMAIN       72    108       LDL-RECEPTOR CLASS A.
FT   DOMAIN      109    205       SRCR.
FT   DOMAIN      217    454       SERINE PROTEASE.
FT   ACT_SITE    257    257       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    304    304       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   ACT_SITE    401    401       CHARGE RELAY SYSTEM (BY SIMILARITY).
FT   SITE        216    217       CLEAVAGE (POTENTIAL).
FT   DISULFID     73     85       BY SIMILARITY.
FT   DISULFID     79     98       BY SIMILARITY.
FT   DISULFID     92    107       BY SIMILARITY.
FT   DISULFID    129    194       BY SIMILARITY.
FT   DISULFID    142    204       BY SIMILARITY.
FT   DISULFID    207    324       BY SIMILARITY.
FT   DISULFID    242    258       BY SIMILARITY.
FT   DISULFID    338    407       BY SIMILARITY.
FT   DISULFID    370    386       BY SIMILARITY.
FT   DISULFID    397    425       BY SIMILARITY.
FT   CARBOHYD    221    221       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1    127       Missing (in isoform B).
FT                                /FTId=VSP_005391.
FT   VARSPLIC    318    454       EMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLN
FT                                HAAVPLISNKICNHRDVYGGIISPSMLCAGYLTGGVDSCQG
FT                                DSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSF
FT                                LDWIHEQMERDLKT -> GTSGSLCGSAALPLFQEDLQLLI
FT                                EAFL (in isoform D).
FT                                /FTId=VSP_005392.
FT   VARSPLIC    261    293       DLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYH -> EIVA
FT                                PRERADRRGRKLLCWRKPTKMKGPRPSHS (in isoform
FT                                T).
FT                                /FTId=VSP_005393.
FT   VARSPLIC    294    454       Missing (in isoform T).
FT                                /FTId=VSP_005394.
FT   VARIANT      53     53       V -> I.
FT                                /FTId=VAR_010781.
FT   VARIANT     103    103       D -> G (in DFNB8/DFNB10).
FT                                /FTId=VAR_013490.
FT   VARIANT     109    109       R -> W (in DFNB8/DFNB10).
FT                                /FTId=VAR_013491.
FT   VARIANT     111    111       G -> S.
FT                                /FTId=VAR_013492.
FT   VARIANT     173    173       D -> N.
FT                                /FTId=VAR_013493.
FT   VARIANT     194    194       C -> F (in DFNB8/DFNB10).
FT                                /FTId=VAR_013494.
FT   VARIANT     251    251       W -> C (in DFNB8/DFNB10).
FT                                /FTId=VAR_011678.
FT   VARIANT     253    253       I -> V (in dbSNP:2839500).
FT                                /FTId=VAR_013101.
FT   VARIANT     404    404       P -> L (in DFNB8/DFNB10).
FT                                /FTId=VAR_011679.
FT   VARIANT     407    407       C -> R (in DFNB8/DFNB10).
FT                                /FTId=VAR_013495.
FT   VARIANT     426    426       A -> T.
FT                                /FTId=VAR_013496.
FT   CONFLICT     46     54       LKFFPIIVI -> FEVFSQSSSL (IN REF. 1).

  Query Match             11.6%;  Score 359;  DB 1;  Length 454;
  Best Local Similarity   33.1%;  Pred. No. 7.1e-17;
  Matches   82;  Conservative   39;  Mismatches  101;  Indels   26;  Gaps    8;

Qy        311 CVACG-----SLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQ 365
              | |||     | |  |       | |||:| |  ||   |||::::   ::|||||
Db        204 CTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWIITAAHCVYDLY 263

Qy        366 APEEWSVGLG-------TRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRP 418
               |: |:: :|         |    ::::: |  |      | |:||: || |:|    ::|
Db        264 LPKSWTIQVGLVSLLDNPAPSHL-VEKIVYHSKYKPKRLGNDIALMKLAGPLTFNEMIQP 322

Qy        419 LCLPYPDHHLPDGE----RGWVLGRARPGAGISS--LQTVPVTLLGPRACSRLHAAPGGD 472
              :||| : : |||:     ||  |    ||| :|  |    | |:  : |:
Db        323 VCLPNSEENFPDGKVCWTSGW--GATEDGAGDASPVLNHAAVPLISNKICNHRDVY---- 376

Qy        473 GSPILPGMVCTS-AVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTA 531
              |  | :| |:|     | : ||:| || ||| : |  | | |  |||  |    :| |:|
Db        377 GGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTR 436

Qy        532 LPAYEDWV 539
              : :: ||:
Db        437 VTSFLDWI 444


Search completed: January  6, 2004, 10:01:45
Job time : 19 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 6, 2004, 09:58:56 ; Search time 40 Seconds
(without alignments)
3683.701 Million cell updates/sec

Title: US-09-978-194A-132
Perfect score: 3108
Sequence: 1 MLLSSLVSLAGSVYLAWILF.....PEPEAEPGSCLANISQPTSC 571

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1868.5	60.1	426	11	Q8CFX9	Q8cfx9 mus musculu
2	724	23.3	766	4	Q8NBY4	Q8nby4 homo sapien
3	481.5	15.5	328	11	Q8BJR6	Q8bjr6 mus musculu
4	451.5	14.5	799	11	Q9DBI0	Q9dbi0 mus musculu
5	448	14.4	327	4	Q8N171	Q8n171 homo sapien
6	447	14.4	284	4	Q8NF86	Q8nf86 homo sapien
7	438.5	14.1	1524	13	Q91674	Q91674 xenopus lae
8	436	14.0	331	11	Q8R1A6	Q8r1a6 mus musculu
9	425	13.7	802	4	Q8IUE2	Q8iue2 homo sapien
10	425	13.7	811	4	Q8IU80	Q8iu80 homo sapien
11	418	13.4	339	11	Q99L44	Q99l44 mus musculu
12	412	13.3	340	11	Q8BJV6	Q8bjv6 mus musculu
13	405	13.0	317	13	Q9DGR3	Q9dgr3 xenopus lae
14	397.5	12.8	297	11	O88781	O88781 rattus ratt
15	394.5	12.7	974	13	Q90WD8	Q90wd8 bufo japoni
16	384.5	12.4	1004	13	P79953	P79953 xenopus lae
17	380	12.2	321	4	Q96RZ8	Q96rz8 homo sapien
18	378	12.2	389	13	Q9PVX7	Q9pvx7 xenopus lae
19	375.5	12.1	812	11	Q9R0W3	Q9r0w3 rattus norv
20	371.5	12.0	812	11	Q91WJ5	Q91wj5 mus musculu
21	369.5	11.9	329	13	O42272	O42272 xenopus lae
22	368.5	11.9	855	11	Q9JJI7	Q9jji7 rattus norv
23	364.5	11.7	334	6	O46507	O46507 papio hamad
24	364	11.7	423	11	Q8BM10	Q8bm10 mus musculu
25	361.5	11.6	422	4	Q8WVC1	Q8wvc1 homo sapien
26	360.5	11.6	810	4	Q15146	Q15146 homo sapien
27	356.5	11.5	371	11	Q8CJ16	Q8cj16 rattus norv
28	356.5	11.5	445	11	Q8CJ17	Q8cj17 rattus norv
29	351	11.3	454	6	O46506	O46506 papio hamad
30	349.5	11.2	453	11	Q8VDE0	Q8vde0 mus musculu
31	349	11.2	624	11	Q9DAT3	Q9dat3 mus musculu
32	348.5	11.2	453	11	Q8K1T0	Q8k1t0 mus musculu
33	347.5	11.2	455	11	Q8CDR0	Q8cdr0 mus musculu
34	345	11.1	581	4	Q9BYE2	Q9bye2 homo sapien
35	344	11.1	667	5	Q9BJM1	Q9bjm1 trichinella
36	343	11.0	335	11	Q8VIF2	Q8vif2 mus musculu
37	343	11.0	624	11	Q91Y47	Q91y47 mus musculu
38	343	11.0	806	6	O18783	O18783 macropus eu
39	342.5	11.0	282	11	Q9D4I3	Q9d4i3 mus musculu
40	342.5	11.0	322	11	Q920S2	Q920s2 mus musculu
41	342.5	11.0	537	4	Q9BYE1	Q9bye1 homo sapien
42	340.5	11.0	624	6	Q95ME7	Q95me7 oryctolagus
43	339	10.9	310	11	Q91XC4	Q91xc4 mus musculu
44	337.5	10.9	471	11	Q8CFE0	Q8cfe0 mus musculu
45	336.5	10.8	490	11	Q920K3	Q920k3 rattus norv

ALIGNMENTS

RESULT 1
Q8CFX9
ID Q8CFX9 PRELIMINARY; PRT; 426 AA.
AC Q8CFX9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to protease, serine, 8 (Prostasin) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC039632; AAH39632.1; -.
KW Protease.
FT NON_TER 1 1
SQ SEQUENCE 426 AA; 45483 MW; 7070BC4E20FAA862 CRC64;

Query Match 60.1%; Score 1868.5; DB 11; Length 426;
Best Local Similarity 80.0%; Pred. No. 2.3e-131;
Matches 339; Conservative 21; Mismatches 63; Indels 1; Gaps 1;

```
Qy      148 ALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSDAPGTLRNLRLRLISRPTCNC 207
            ||||| |||  | |||||| : |||||||||||||||:|||   ||||||||||||||||
Db        4 ALLQLTHPTVQTTLCLPQPTYHFPFGASCWATGWDQNTSDVSRTLRNLRLRLISRPTCNC 63

Qy      208 IYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSC 267
            :||:|||| ||||||||||||| ||| ||||||||||||:| |||||||| ||||| | |
Db       64 LYNRLHQRLLSNPARPGMLCGGAQPGEQGPCQGDSGGPVMCREPDGHWVQVGIISFTSKC 123

Qy      268 AQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAP 327
            |||| |||||: | ||||||| |  |||| |:|   :||||:|||||||||:|||||||
Db      124 AQEDTPVLLTDMAVHSSWLQAHVHEAAFLVQAPGVVKMSDENSCVACGSLRSAGPQAGAL 183

Qy      328 SPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLI 387
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Db        184 SQWPWDARLKHHGKLACGGALVSEVVVLTAAHCFIGRQTLEEWSVGLGAGPEEWGLKQLI 243

Qy        388 LHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGIS 447

Db        244 LHGAYTHPEGGYDVAFLLLAQPVTLGPGLRPLCLPYADHHLPDGEHGWVLGLTQK-AGIN 302

Qy        448 SLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLSGAPLVHEVRGT 507

Db        303 YPQTVPVTVLGPMACSRQHAAPGGTGIPILPGMVCTTVVGEPPHCEGLSGAPLVHEIRGT 362

Qy        508 WFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPGSCLANISQ 567

Db        363 WFLVGLHSFGDTCQSSAKPAVFAALSAYEDWISNLDWQVYFAEEPEPEAETGSCLVNSSQ 422

Qy        568 PTSC 571

Db        423 PASC 426
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RESULT 2
Q8NBY4
ID Q8NBY4 PRELIMINARY; PRT; 766 AA.
AC Q8NBY4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90661.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK075142; BAC11431.1; -.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 3.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPc; 3.
DR PROSITE; PS50240; TRYPSIN_DOM; 3.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 766 AA; 82564 MW; 3630D550CB06BD55 CRC64;

Query Match 23.3%; Score 724; DB 4; Length 766;
Best Local Similarity 35.4%; Pred. No. 1.1e-45;
Matches 179; Conservative 68; Mismatches 189; Indels 70; Gaps 18;

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Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTT----HTPLCL 163

Db         12 WSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCL 71

Qy        164 PQPAHRFPFGASCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSN 219

Db         72 PRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTL 131

Qy        220 PARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNT 279

Db        132 QILPGMLCAGYPEGRRDTCQGDSGGPLVC-EEGGRWFQAGITSFGFGCGRRNRPGVFTAV 190

Qy        280 AAHSSWLQARVQGA----AFLAQSPET---PEMSDEDSCV----ACGSLRTAGPQAGAPS 328

Db        191 ATYEAWIREQVMGSEPGPAFPTQPQKTQSDPQEPREENCTIALPECG-------KAPRPG 243

Qy        329 PWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEE-------WSVGLGTRPEEW 381

Db        244 AWPWEAQVMVPGSRPCHGALVSESWVLAPASCFLDPNSSDSPPRDLDAWRVLLPSRPRAE 303

Qy        382 GLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGER----GWVL 437

Db        304 RVARLVQHENASW-DNASDLALLQLRTPVNLSAASRPVCLPHPEHYFLPGSRCRLARW-- 360

Qy        438 GRARPGAGISSLQTVPVTLLGPRACSRLHAAPGG----DGSPILPGMVCTS--AVGELPS 491

Db        361 GRGEPALGPGAL--LEAELLGGWWCHCLYGRQGAAVPLPGDP--PHALCPAYQEKEEVGS 416

Qy        492 CEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYF--- 548

Db        417 CWNDSRWSLLCQEEGTWFLAGIRDFPSGC---LRPRAFFPLQTHGPWISHVTRGAYLEDQ 473

Qy        549 --------AEEPE-----PEAEPGSC 561

Db        474 LAWDWGPDGEETETQTCPPHTEHGAC 499
```

RESULT 3
Q8BJR6
ID Q8BJR6 PRELIMINARY; PRT; 328 AA.
AC Q8BJR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to MARAPSIN precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK080281; BAC37864.1; -.
SQ SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;

Query Match 15.5%; Score 481.5; DB 11; Length 328;
Best Local Similarity 36.1%; Pred. No. 5e-28;
Matches 99; Conservative 46; Mismatches 112; Indels 17; Gaps 6;

```
Qy         60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119

Db         43 NALEGEWPWQVSIQRNGIHFCGGSLIAPTWVLTAAHCFSN--TSDISIYQVLLGALKLQQ 100

Qy        120 LSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175

Db        101 PGPHALYVPVKQVKSNPQYQGMASSADVALVELQGPVTFTNYILPVCLPDPSVIFESGMN 160

Qy        176 CWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQ-LHQRHLSNPARPGMLCGGP 230

Db        161 CWVTGWGSPSEQDRLPNPRVLQKLAVPIIDTPKCNLLYNKDVESDFQLKTIKDDMLCAGF 220

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARV 290

Db        221 AEGKKDACKGDSGGPLVCL-VDQSWVQAGVISWGEGCARRNRPGVYIRVTSHHKWIHQII 279

Qy        291 QGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQA 324

Db        280 PELQFQGRAGTQQQQKDSQ-----GQQRLAGNSA 308
```

RESULT 4
Q9DBI0

```
ID   Q9DBI0      PRELIMINARY;      PRT;   799 AA.
AC   Q9DBI0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   1300008A22Rik protein (RIKEN cDNA 1300008A22 gene).
GN   TMPRSS6 OR 1300008A22RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; AK004939; BAB23684.1; -.
DR   EMBL; BC029645; AAH29645.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.308; -.
DR   MGD; MGI:1919003; Tmprss6.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000859; CUB_domain.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00057; ldl_recept_a; 2.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   PROSITE; PS01180; CUB; 1.
DR   PROSITE; PS01209; LDLRA_1; 1.
DR   PROSITE; PS50068; LDLRA_2; 3.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   799 AA;  89557 MW;  16315A646A4D5288 CRC64;

  Query Match             14.5%;  Score 451.5;  DB 11;  Length 799;
  Best Local Similarity   37.6%;  Pred. No. 2.5e-25;
  Matches   92;  Conservative   40;  Mismatches   96;  Indels   17;  Gaps    5;

Qy         52 QGKAKR-HGNTV--PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSW 108
              || : |  | ||   |||||||:: :| ||| |:|:|| ||:|||||:: :      |
Db        559 QGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFQEDSMASPKLW 618

Qy        109 SVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLP 164
              :| || :::    ||     |: | |   :   |  |:||||| ||  ::    |:|||
Db        619 TVFLGKMRQNSRWPGEVSFKVSRLFLHPYHEEDSHDYDVALLQLDHPVVYSATVRPVCLP 678

Qy        165 QPAHRFPFGASCWATGWDQDTSDAP--GTLRNLRLRLISRPTCNCIYNQLHQRHLSNPAR 222
              :| |  |  || |||       |   ||: : ::|: :  |:  |
Db        679 ARSHFFEPGQHCWITGWGAQREGGPVSNTLQKVDVQLVPQDLCSEAYRY--------QVS 730

Qy        223 PGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAH 282
              | ||| | : | :  ||||||||::| || | ||::|:   | : :   : |
Db        731 PRMLCAGYRKGKKDACQGDSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRV 790

Qy        283 SSWLQ 287
              :|:|
Db        791 INWIQ 795


RESULT 5
Q8N171
ID   Q8N171      PRELIMINARY;      PRT;   327 AA.
AC   Q8N171;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to protease, serine, 8 (Prostasin) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; BC036846; AAH36846.1; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
FT   NON_TER       1      1
SQ   SEQUENCE   327 AA;  35106 MW;  60458ED817AC1CF3 CRC64;

  Query Match             14.4%;  Score 448;  DB 4;  Length 327;
  Best Local Similarity   41.0%;  Pred. No. 1.6e-25;
  Matches  100;  Conservative   32;  Mismatches   84;  Indels   28;  Gaps    7;

Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
              ||||||||:: :|||:| |||:|  ||||||||| : |     : | ||:|:    ||
Db         93 GEWPWQASIQHRGAHVCGGSLIAPQWVLTAAHCFPRRALPA--EYRVRLGALRLGSTSPR 150

Qy        124 AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT 179
                | |  : ||  |:       |||||||  |   :    |:||| |  | | |  | |
Db        151 TLSVPVRRVLLPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRVT 210

Qy        180 GWDQDTSDAPGT-------LRNLRLRLISRPTCNCIYN------QLHQRHLSNPARPGML 226
              ||    |  ||         |: :|: |:   ||: :|:      |  :  |     || |
Db        211 GWG---SLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERIVL-----PGSL 262

Qy        227 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
              | |   | :  ||||||||: ||:  | ||  |::|:   ||  : | : |: | :| |:
Db        263 CAGYPQGHKDACQGDSGGPLTCLQ-SGSWVLVGVVSWGKGCALPNRPGVYTSVATYSPWI 321

Qy        287 QARV 290
              ||||
Db        322 QARV 325


RESULT 6
Q8NF86
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ID   Q8NF86      PRELIMINARY;      PRT;   284 AA.
AC   Q8NF86;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Serine protease EOS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Darrow A.L., Qi J., Andrade-Gordon P., Chen C.;
RT   "DNA encoding the human serine protease EOS.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; AF536382; AAN04055.1; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   284 AA;  30110 MW;  FDF3F1750D569978 CRC64;

  Query Match             14.4%;  Score 447;  DB 4;  Length 284;
  Best Local Similarity   40.7%;  Pred. No. 1.6e-25;
  Matches  101;  Conservative   31;  Mismatches   88;  Indels   28;  Gaps    7;

Qy         64 GEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPG 123
              ||||||||::  |||:| |||:|  |||||||||  : |      : | ||:|:    ||
Db         46 GEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRALPA--EYRVRLGALRLGSTSPR 103

Qy        124 AEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWAT 179
                | |  : ||  |:       |||||||  |   :    |:||| |  | | |  | |
Db        104 TLSVPVRRVLLPPDYSEDGARGDLALLQLRRPVPLSARVQPVCLPVPGARPPPGTPCRVT 163

Qy        180 GWDQDTSDAPGT-------LRNLRLRLISRPTCNCIYN------QLHQRHLSNPARPGML 226
              ||    |  ||        |: :|: |:   ||: :|:      |  :  |     || |
Db        164 GWG---SLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERIVL-----PGSL 215

Qy        227 CGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWL 286
              | |   | :  |||||||: ||:  | ||  |::|:   ||  : | : |: | :| |:
Db        216 CAGYPQGHKDACQGDSGGPLTCLQ-SGSWVLVGVVSWGKGCALPNRPGVYTSVATYSPWI 274

Qy        287 QARVQGAA 294
              ||||  |
Db        275 QARVTSNA 282


RESULT 7
Q91674
ID   Q91674      PRELIMINARY;      PRT;  1524 AA.
AC   Q91674;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Polyprotein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99432219; PubMed=10500163;
RA   Lindsay L.L., Yang J.C., Hedrick J.L.;
RT   "Ovochymase, a Xenopus laevis egg extracellular protease, is
RT   translated as part of an unusual polyprotease.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yang J.C., Lindsay L.L., Hedrick J.L.;
RT   "cDNA Cloning of Ovochymase, a Chymotrypsin-like Protease Released
RT   From Xenopus laevis Eggs at Fertilization.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: CONTAINS 4 CUB DOMAINS.
DR   EMBL; U81290; AAC24717.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.022; -.
DR   MEROPS; S01.245; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000859; CUB_domain.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00431; CUB; 5.
DR   Pfam; PF00089; trypsin; 3.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00042; CUB; 4.
DR   SMART; SM00020; Tryp_SPc; 3.
DR   PROSITE; PS01180; CUB; 5.
DR   PROSITE; PS50240; TRYPSIN_DOM; 3.
DR   PROSITE; PS00134; TRYPSIN_HIS; 3.
DR   PROSITE; PS00135; TRYPSIN_SER; 3.
KW   Hydrolase; Protease; Serine protease.
FT   CHAIN        57    308       SERINE PROTEASE.
FT   CHAIN       584    817       SERINE PROTEASE.
FT   CHAIN      1295   1524       OVOCHYMASE.
SQ   SEQUENCE   1524 AA;  167566 MW;  32EFE42128F37268 CRC64;

  Query Match             14.1%;  Score 438.5;  DB 13;  Length 1524;
  Best Local Similarity   18.8%;  Pred. No. 4.9e-24;
  Matches  147;  Conservative   97;  Mismatches  211;  Indels  327;  Gaps   20;

Qy         59 GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE 118
              |:   |  ||  |::    ||| ||:|    |:|||||       :::  :|::|   ::
Db         61 GDAAVGGQPWTVSLKLNERHICGGSIVRKDMVVTAAHCVYPVTEIKVSHMTVIVGEYDQQ 120

Qy        119 GLSPGAEEVGVAALQ-LPRAYNHYSQGSDLALLQLAHP----TTHTPLCLPQPAHRFPFG 173
                :    : : |: :: |       : | :|:|: |: |     :   |:|||   :   |
Db        121 VMDSQEQSIPVSHIEPHPNYRGDGNMGYDIALVFLSKPIIFGSQVQPICLPQVGEKIEAG 180

Qy        174 ASCWATGWD--QDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQ 231
              | ::||   ::  |    |: ::| ::   ||: :  :    | :   |||| |
Db        181 TLCVSSGWGRLEENGDLSPVLQEVKLPVVDNGTCHAVLEPIGHPVLDDT----MLCAGFP 236

Qy        232 PGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSC-----------AQEDAPVLLTN-- 278
              |    |||||||| :|    | |  || :|:   |           :|  :| : :
Db        237 EGGMDACQGDSGGPFVCRRRSGVWFLAGCVSWGLGCGRSWGAKQIIRSQSGSPAIFSRVS 296

Qy        279 -----------TAAHSS--------------------------WLQA------------ 288
                        |   ||                        |: |
Db        297 SVLDFLRPPKLTGGCSSKGRTITGKNGTVRYPLSGNYSINSVCRWMLAVQKAKTIEIRFL 356

Qy        289 ------------------------------------------------------------ 288

Db        357 QLDIEDHATCTFDYLSFTVNEKMIRKVCGSTIPSPLIVRSNKVTVTFFSDGTFTGRGFEI 416

Qy        289 ----------------------------------RVQGAAFLAQSPET----------- 302
                                               |::  ::: ::||
Db        417 QFLAIPTKAASACGSAKILKKKGMIYSPNYPDPYPRLKTCSWIIEAPENHIVKLKFEDFN 476

Qy        303 --------------------------------PEMSDEDSCV---------------- 312
                                             |  | |:: :
Db        477 VEYGHGCIYDAVEVYDGAEEKQLIARLCGYTLPLPISSPENTMLIRFKTDMENSYPGFKV 536

Qy        313 ------------------------------ACGSL---------RTAGPQAGAPSPWP 331
                                           ||            |  | :  :|: ||
Db        537 KFSFVPKEKQFSLPVDDTPTISMLHPRAIALDVCGMAPMTPKWWLPRIVGGEEASPNSWP 596

Qy        332 WEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLG--------TRPEEWGL 383
              |: ::       | ||::| : :|||||| |    |  |:|  |       : :   :
Db        597 WQVQIFFLRTFHCEGAIISPQWILTAAHC-IRAAEPSYWTVIAGDHNRMLNESTEQIRNI 655
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Qy        384 KQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE----RGW--VL 437
Db        656 KTIRIHDNYNSETYDNDIALLYLEEPLDLNDFVRPVCLPEPEEVLTPASVCVVTGWGNTA 715

Qy        438 GRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAV--GEL------ 489
Db        716 EDGQPALGLQQLQL----------------------PILDSIICNTSYYSGELTDHMLC 752

Qy        490 ---PS------CEGLSGAPLVHEVRGTWF-LAGLHSFGDACQGPARPAVFTALPAYEDWV 539
Db        753 AGFPSSKEKDACQGDSGGPLVCQNEKEQFSIYGLVSWGEGCGRVSKPGVYTKVRLFFTWI 812

Qy        540 SS 541
Db        813 QN 814
```

RESULT 8
Q8R1A6
ID Q8R1A6 PRELIMINARY; PRT; 331 AA.
AC Q8R1A6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RIKEN cDNA 2010001P08 gene.
GN 2010001P08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC024903; AAH24903.1; -.
DR HSSP; P00761; 1AN1.
DR MGD; MGI:1917064; 2010001P08Rik.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; Tryp_SPc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 331 AA; 35639 MW; C06F6EF2FA261636 CRC64;

Query Match 14.0%; Score 436; DB 11; Length 331;
Best Local Similarity 35.9%; Pred. No. 1.2e-24;
Matches 98; Conservative 47; Mismatches 102; Indels 26; Gaps 9;

```
Qy         53 GKAKRHGNTVPGE------WPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELN 106
Db         46 GRPRTSGRIVSGQDAQLGRWPWQVSVRENGAHVCGGSLIAEDWVLTAAHCFNQGQS--LS 103

Qy        107 SWSVVLGSLQREGLSPGAEEVGVAA--LQLPR-AYNHYSQGSDLALLQLAHPTTHT---- 159
Db        104 IYTVLLGTISSYPEDNEPKELRAVAQFIKHPSYSADEHSSG-DIALVQLASPISFNDYML 162

Qy        160 PLCLPQPAHRFPFGASCWATGWDQDTSD----APGTLRNLRLRLISRPTCNCIYNQLHQR 215
Db        163 PVCLPKPGDPLDPGTMCWVTGWGHIGTNQPLPPPFTLQELQVPLIDAETCNTYYQENSIP 222

Qy        216 HLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVL 275
Db        223 GTEPVILEGMLCAGFQQGKKDACNGDSGGPLVC-DINDVWIQAGVVSWGSDCALFKRPGV 281

Qy        276 LTNTAAHSSWLQ-----ARVQGAAFLAQSPETP 303
Db        282 YTNVSVYISWIQNTMWNLPMEGRGFSPSLSGTP 314
```

RESULT 9
Q8IUE2
ID Q8IUE2 PRELIMINARY; PRT; 802 AA.
AC Q8IUE2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Matriptase-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22241917; PubMed=12149247;
RA Velasco G., Cal S., Quesada V., Sanchez L.M., Lopez-Otin C.;
RT "Matriptase-2, a membrane-bound mosaic serine proteinase predominantly
RT expressed in human liver and showing degrading activity against
RT extracellular matrix proteins.";
RL J. Biol. Chem. 277:37637-37646(2002).
DR EMBL; AJ319876; CAC85953.1; -.
SQ SEQUENCE 802 AA; 88901 MW; C30D37BEC4F1D22E CRC64;

Query Match 13.7%; Score 425; DB 4; Length 802;
Best Local Similarity 35.4%; Pred. No. 2.3e-23;
Matches 87; Conservative 39; Mismatches 106; Indels 14; Gaps 3;

```
Qy         48 VQEPQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
Db        561 LQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL 620

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCL 163
Db        621 WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCL 680

Qy        164 PQPAHRFPFGASCWATGWDQDTSDAP--GTLRNLRLRLISRPTCNCIYNQLHQRHLSNPA 221
Db        681 PARSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEVYRY--------QV 732

Qy        222 RPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAA 281
Db        733 TPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITG 792

Qy        282 HSSWLQ 287
Db        793 VISWIQ 798
```

RESULT 10
Q8IU80
ID Q8IU80 PRELIMINARY; PRT; 811 AA.
AC Q8IU80;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type II transmembrane serine protease 6.
GN TMPRSS6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hooper J.D., Quigley J.P.;
RT "TMPRSS6, a new type II transmembrane serine protease.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY055383; AAL16413.1; -.
DR EMBL; AY055384; AAL16414.1; -.
KW Protease; Transmembrane.
SQ SEQUENCE 811 AA; 89999 MW; 7EEF193F655DDE9D CRC64;

Query Match 13.7%; Score 425; DB 4; Length 811;

```
  Best Local Similarity   35.4%;  Pred. No. 2.4e-23;
  Matches   87;  Conservative   39;  Mismatches  106;  Indels   14;  Gaps    3;

Qy         48 VQEPQGKAKRHGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNS 107
              :| |  :     :  |||||||:: :| ||| |:|:|| ||:||||||:: :
Db        570 LQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL 629

Qy        108 WSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCL 163
              |:| || : :   ||     |: | |   :   |  |:|||| ||   :    |:||
Db        630 WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCL 689

Qy        164 PQPAHRFPFGASCWATGWDQDTSDAP--GTLRNLRLRLISRPTCNCIYNQLHQRHLSNPA 221
              |  :| |  |  || |||       |    |: : ::|| :  |: :|
Db        690 PARSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEVYRY--------QV 741

Qy        222 RPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAA 281
              | ||| | : | :  ||||||||::|    | |  ||::|:   | : :   : |
Db        742 TPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITG 801

Qy        282 HSSWLQ 287
              ||:|
Db        802 VISWIQ 807


RESULT 11
Q99L44
ID   Q99L44      PRELIMINARY;      PRT;   339 AA.
AC   Q99L44;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to protease, serine, 8 (Prostasin).
GN   PRSS8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ, and Swiss; TISSUE=Lung;
RA   Verghese G.M., Caughey G.H.;
RT   "Molecular cloning and characterization of mouse prostasin, a type I
RT   membrane-associated serine protease of the gamma-tryptase/prostasin
RT   gene family.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Kitamura K., Takefumi N., Kimio T.;
RT   "mouse serine protease.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR   EMBL; BC003851; AAH03851.1; -.
DR   EMBL; AF378086; AAL06320.1; -.
DR   EMBL; AF378085; AAL06319.1; -.
DR   EMBL; AB038244; BAB82496.1; -.
DR   HSSP; P00734; 1UVS.
DR   MGD; MGI:1923810; Prss8.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   339 AA;  36216 MW;  BC2DE88BC057AF10 CRC64;

  Query Match             13.4%;  Score 418;  DB 11;  Length 339;
  Best Local Similarity   35.6%;  Pred. No. 2.8e-23;
  Matches   93;  Conservative   41;  Mismatches  101;  Indels   26;  Gaps    6;

Qy         59 GNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQRE 118
              |:  ||:|||| |:   | |:| |||:: ||::|||||  :  : |  :: | ||: | :
Db         49 GSAKPGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGAHQLD 106

Qy        119 GLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGA 174
                 |       || :    :|       |:||::|: | | :    |:|||     || |
Db        107 SYSNDTVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGL 166

Qy        175 SCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGP 230
              |  |||       :   |  |: | : |||| ||:|:||       :  :  ||| |
Db        167 HCTVTGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGY 226

Qy        231 QPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW----- 285
              | :  ||||||||: |   :| |  |||:|:  :|   : | : | |: ::||
Db        227 VKGGKDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV 285

Qy        286 --LQARVQGAAFLAQSPETPE 304
                || ||         |:| |
Db        286 AELQPRV--------VPQTQE 298


RESULT 12
Q8BJV6
ID   Q8BJV6      PRELIMINARY;      PRT;   340 AA.
AC   Q8BJV6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Prostasin.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Eye;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK078696; BAC37362.1; -.
SQ   SEQUENCE   340 AA;  36503 MW;  3C2540E9B3A81C8A CRC64;

  Query Match             13.3%;  Score 412;  DB 11;  Length 340;
  Best Local Similarity   35.8%;  Pred. No. 7.9e-23;
  Matches   92;  Conservative   39;  Mismatches  100;  Indels   26;  Gaps    6;

Qy         63 PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSP 122
              ||:|||| |:   | |:| ||||:: ||::||||| :  : |  :: | ||  | :  |
Db         54 PGQWPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE--AYEVKLGDHQLDSYSN 111

Qy        123 GAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGASCWA 178
                  || :    :|       |:||::|: | | :    |:|||     || |  |
Db        112 DTVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTV 171

Qy        179 TGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGV 234
              |||       :   |  |: | : |||| ||:|:||       :  :  ||| |   |
Db        172 TGWGHVAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGG 231

Qy        235 QGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSW-------LQ 287
              :  |||||||: |   :| |  |||:|:  :|   : | : | |: ::||       ||
Db        232 KDACQGDSGGPLSC-PMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHVAELQ 290

Qy        288 ARVQGAAFLAQSPETPE 304
               ||         |:| |
Db        291 PRV--------VPQTQE 299
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RESULT 13
Q9DGR3
ID   Q9DGR3      PRELIMINARY;      PRT;   317 AA.
AC   Q9DGR3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Embryonic serine protease-1.
GN   XESP-1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20363741; PubMed=10903452;
RA   Yamada K., Takabatake T., Takeshima K.;
RT   "Isolation and characterization of three novel serine protease genes
RT   from Xenopus laevis.";
RL   Gene 252:209-216(2000).
DR   EMBL; AB038496; BAB08216.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.048; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   317 AA;  34413 MW;  EEC78A9F46D138FE CRC64;

  Query Match             13.0%;  Score 405;  DB 13;  Length 317;
  Best Local Similarity   33.2%;  Pred. No. 2.4e-22;
  Matches   89;  Conservative   45;  Mismatches  106;  Indels   28;  Gaps    7;

Qy         60 NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREG 119
              :|  | |||| |:   |:||| ||:::| |:||| || |       :   | ||: |
Db         46 DTRQGAWPWQVSLEFNGSHICGGSIISDQWILTATHCIEHPDLP--SGCGVRLGAYQLYV 103

Qy        120 LSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHT----PLCLPQPAHRFPFGAS 175
               :|    | |  : :   :|       |:|||:|: |    |    |:|||      |  |
Db        104 KNPHEMTVKVDIIYINSEFNGPGTSGDIALLKLSSPIKFTEYILPICLPASPVTFSSGTE 163

Qy        176 CWATGWDQDTSDA----PGTLRNLRLRLISRPTCNCIYNQLHQRHLSNP-------ARPG 224
              || ||| |  |:      | ||: : :|:| :|  :|      |:::       :
Db        164 CWITGWGQTGSEVPLQYPATLQKVMVPIINRDSCEKMY------HINSVISETEILIQSD 217

Qy        225 MLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS 284
               :| | | | :  |||||||::| :  | | ||||:|:   || :: | : |    |: :
Db        218 QICAGYQAGQKDGCQGDSGGPLVC-KIQGFWYQAGIVSWGERCAAKNRPGVYTFVPAYET 276

Qy        285 WLQARVQGAAFLAQSPETPEMSDEDSCV 312
              |: |    : ::  | |   |   | |
Db        277 WISER----SVISFKPFTSSSSPSSSSV 300


RESULT 14
O88781
ID   O88781      PRELIMINARY;      PRT;   297 AA.
AC   O88781;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Serine protease precursor (Fragment).
GN   BSP2.
OS   Rattus rattus (Black rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10117;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Fisher; TISSUE=Brain;
RX   MEDLINE=98389725; PubMed=9722524;
RA   Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe R.;
RT   "Serine Proteases in Rodent Hippocampus.";
RL   J. Biol. Chem. 273:23004-23011(1998).
DR   EMBL; AJ005642; CAA06644.1; -.
DR   HSSP; P00763; 1DPO.
DR   MEROPS; S01.252; -.
DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00089; trypsin; 1.
DR   SMART; SM00020; Tryp_SPc; 1.
DR   PROSITE; PS50240; TRYPSIN_DOM; 1.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     23       POTENTIAL.
FT   CHAIN         24    297       SERINE PROTEASE.
SQ   SEQUENCE   297 AA;  32086 MW;  6DA25C6633D6AB55 CRC64;

  Query Match             12.8%;  Score 397.5;  DB 11;  Length 297;
  Best Local Similarity   34.2%;  Pred. No. 8.2e-22;
  Matches   92;  Conservative   47;  Mismatches  105;  Indels   25;  Gaps    9;

Qy         53 GKAKRHGNTVPGE------WPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELN 106
              || ::    | ||      |||  |: : |:| |:|||: : ||::|||||  :   : :
Db         32 GKPQQLNRVVGGEDSADAQWPWIVSILKNGSHHCAGSLLTNRWVVSAAHCF-SSNMDKPS 90

Qy        107 SWSVVLGSLQREGLSPGAEEVGVAA-LQLPRAYNHYSQGSDLALLQLAHPTTHT----PL 161
               :||:||: :     | :::||:|: |  ||        :|:||::|  |   :    |:
Db         91 PYSVLLGAWKLGNPGPRSQKVGIASVLPHPRYSRKEGTHADIALVRLERPIQFSERILPI 150

Qy        162 CLPQPAHRFPFGASCWATGW----DQDTSDAPGTLRNLRLRLISRPTCNCIYNQLHQRHL 217
              |||  :   |   :||  ||     |       | ||: |:: :|    |  :|     |
Db        151 CLPDSSVHLPPNTNCWIAGWGSIQDGVPLPRPQTLQKLKVPIIDPELCKSLY----WRGA 206

Qy        218 SNPA-RPGMLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLL 276
              |    ||| |   | :  | |||||::| : | ||:  ||||:   ||: : | :
Db        207 GQEAITEDMLCAGYLEGKRDACLGDSGGPLMC-QVDDHWLLTGIISWGEGCAERNRPGVY 265

Qy        277 TNTAAHSSWLQARVQGAAF---LAQSPET 302
              |:  ||  |:|  |||      || | :|
Db        266 TSLLAHRPWVQRIVQGVQLRGRLADSGDT 294


RESULT 15
Q90WD8
ID   Q90WD8      PRELIMINARY;      PRT;   974 AA.
AC   Q90WD8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Oviductin.
OS   Bufo japonicus (Japanese toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Bufo.
OX   NCBI_TaxID=8387;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=oviductal pars recta;
RA   Hiyoshi M., Takamune K., Mita K., Kubo H., Sugimoto Y., Katagiri C.;
RT   "Oviductin, the oviductal protease that mediates gamete interaction by
RT   affecting the vitelline envelope in Bufo japonicus: Its molecular
RT   cloning and analyses of expression and post-translational
RT   activation.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC   -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR   EMBL; AB070367; BAB63372.1; -.
DR   HSSP; P00761; 1AN1.
DR   MEROPS; S01.240; -.
DR   InterPro; IPR001314; Chymotrypsin.
DR   InterPro; IPR000859; CUB_domain.
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DR   InterPro; IPR001254; Ser_protease_Try.
DR   Pfam; PF00431; CUB; 2.
DR   Pfam; PF00089; trypsin; 2.
DR   PRINTS; PR00722; CHYMOTRYPSIN.
DR   SMART; SM00042; CUB; 2.
DR   SMART; SM00020; Tryp_SPc; 2.
DR   PROSITE; PS01180; CUB; 2.
DR   PROSITE; PS50240; TRYPSIN_DOM; 2.
DR   PROSITE; PS00134; TRYPSIN_HIS; 1.
DR   PROSITE; PS00135; TRYPSIN_SER; 1.
KW   Hydrolase; Protease; Serine protease.
SQ   SEQUENCE   974 AA;  107647 MW;  F19705A470465553 CRC64;

  Query Match             12.7%;  Score 394.5;  DB 13;  Length 974;
  Best Local Similarity   19.5%;  Pred. No. 5.5e-21;
  Matches  162;  Conservative   83;  Mismatches  213;  Indels  373;  Gaps   26;

Qy         46 RKVQEPQGKAKRHG--------------------NTVPGEWPWQASVRRQGAHICSGSL 84
              | | :  |:  | |                    : | || ||  |::| | | | |::
Db         20 RGVTDSPGRVSRCGERPAANTSVSYGLLSRIVGGTSAVKGESPWMVSLKRDGKHFCGGTI 79

Qy         85 VADTWVLTAAHC-------FEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLP-- 135
              ::| :|||||||       |: : :   : ::|   | ||  :          :  : |
Db         80 ISDKYVLTAAHCVLEKNFEFQVSVSIGDHDFAVYERSEQRFAIK--------SVFKHPNF 131

Qy        136 ---RAYNHYSQGSDLALLQLAHPTTH----TPLCLPQPAHRFPFGASCWATGWD--QDTS 186
                 | :|:     |||:|:|    |       | ||| |   || |  | | ||   |:
Db        132 KPSRPFNY-----DLAILELVESITFDKDIQPACLPSPDDVFPTGTLCMALGWGRLQENG 186

Qy        187 DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPV 246
              | :|: : | ||     |  |   : :|     |   ::| |   | :  ||||||||
Db        187 RLPSSLQKVVLPLIEYRRCLSIMETVDRR----LAFETVVCAGFPEGGKDACQGDSGGPF 242

Qy        247 LCLEPDGHWVQAGIISFASSCAQ---------------------------------EDA 272
              ||    | ||  |: |:   ||:                                 :|
Db        243 LCQRSQGRWVLVGVTSWGLGCARKWADNILDPVESKGSPGVFTDIQRLLNWLSENLNQDK 302

Qy        273 P-----------------------------------------------VLLT----- 277
              |                                              :|||
Db        303 PDFPTYQVQCSTNDGIEKGTTGEILLPTGYKKYYSNNEKCIWTIIVPRGKHILLTFKSFN 362

Qy        278 ------------------------------------------------------------ 277

Db        363 VECDYSCDLDYLVIYSALGRLIGKFCGDVSPRPLLIADASITLKFISDFHEYKTGFSLFY 422

Qy        278 ----------------------------------NTAAHSSW----------------- 285
                                               :: |:  |
Db        423 EAVEPDTYPDSDCGSVAVIFEEGEIQTMNHPHLYSSHANCQWVVHSPANYIIKITFLVFE 482

Qy        286 ----------------LQARVQGAAF--------------------------------- 295
                              ||  |    |
Db        483 VEPSEGCIFDRLVVYHDLQGTVVAGFFCGFALPDPVLSVSNVMQITFTSDYSANYLGFRA 542

Qy        296 -----LAQSPETPE------MSDEDSC----VACGSLRTAGP-------------QAGAP 327
                  |  ||  ||        ::|:       ||      |             :   |
Db        543 VISFVLPSSPVKPEKGNNQPRKNQDAMQHFDEGCG----VSPLPPRFLYHNLIKAEEAMP 598

Qy        328 SPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQA-PE-----------EWSVGLG 375
              : |||   :    :  | ||::|:  |:|:|:|   |:  |             | |:
Db        599 NSWPWHVSINFGNKHVCNGAILSKTFVVTSANCVADREEFPSIGLIVAGLHDLESSINTQ 658

Qy        376 TRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGE--- 432
              || |:    :|:|  |       ||:||: : :|    : ::|:|||     |   :
Db        659 KRPVEY----VIVHPDYNRLSKDYDVALIHVQRPFQYNSYVQPICLPDGHSRLEPSKLCV 714

Qy        433 -RGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGE--L 489
               || |          : || : | :|    | : :     ||  |   | |   : |
Db        715 VSGWDLNVELS----TKLQQLEVPVLMDDVCKKYY-----DG--ITDRMFCAGVIAEEDN 763

Qy        490 PSCEGLSGAPLV-HEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWV 539
               ||   ||||||     ||: : |: | |  |    :  |:::  :  |:
Db        764 ASCLAQSGAPLVCQSAPGTYAIFGIVSRGVGCNETPKAGVYSSVFLFIPWI 814
```

Search completed: January 6, 2004, 10:02:38
Job time : 43 secs